

## STIC Search Report Biotech-Chem Library

## STIC Database Tracking Number:107949

TO: Terra Gibbs

Location: cm1/12a12/11e12

Art Unit: 1635

Sunday, November 16, 2003

Case Serial Number: 10/005337

From: Toby Port

**Location: Biotech-Chem Library** 

CM1-6A04

Phone: 308-3534

toby.port@uspto.gov

## Search Notes

Dear Examiner Gibbs,

Here are the results of your search.

Please feel free to contact me if you have any questions.

**Toby Port** 



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# STIC SEARCH RESULTS FEEDBACK FORM

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Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

Voluntary Results Feedback Form
> I am an examiner in Workgroup: Example: 1610
> Relevant prior art found, search results used as follows:
☐ 102 rejection
☐ 103 rejection
☐ Cited as being of interest.
Helped examiner better understand the invention.
Helped examiner better understand the state of the art in their technology.
Types of relevant prior art found:
☐ Foreign Patent(s)
<ul> <li>Non-Patent Literature         <ul> <li>(journal articles, conference proceedings, new product announcements etc.)</li> </ul> </li> </ul>
> Relevant prior art not found:
Results verified the lack of relevant prior art (helped determine patentability).
Results were not useful in determining patentability or understanding the invention.
Comments:

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### STIC-Biotech/ChemLib

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Gibbs, Terra

Sent: To: Subject: Sunday, November 09, 2003 2:54 PM STIC-Biotech/ChemLib Sequence search request...

RECEIVED

Could you please do a regular search of SEQ ID NOs: 1 and 2 of USSN 10/005337?

(STIC)

Also could you please search do an oligomer search SEQ ID NOs: 1 and 2, length limited to 50 nucleobases or less.

Thank You.

Terra Cotta Gibbs, Ph.D. Art Unit 1635 CM1, 12A12 703-306-3221

Searcher:	
Phone:	
Location:	
Date Picked Up:	
Date Completed:	
Searcher Prep/Review:	
Clerical:	
Online time:	

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

/ENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

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# STIC SEARCH RESULTS FEEDBACK FORM

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

Voluntary Results Feedback Form
> I am an examiner in Workgroup: Example: 1610
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☐ Foreign Patent(s)
<ul> <li>Non-Patent Literature         <ul> <li>(journal articles, conference proceedings, new product announcements etc.)</li> </ul> </li> </ul>
> Relevant prior art <b>not found:</b>
Results verified the lack of relevant prior art (helped determine patentability).
Results were not useful in determining patentability or understanding the invention.
Comments:

Drop offior send completed forms to STIC/Blotech-Chem Library GMI — Circ. Desk



masn May 18 394d SHL

## Schreiber, David

From:

Gibbs, Terra

Sent:

Sunday, November 09, 2003 2:52 PM

To:

Schreiber, David

Subject:

Sequence search request...

Hi David, I have a sequence search request.

NO CRF

The request is for % identity of SEQ ID NOs: 1 and 2 of USSN 10/005337 to SEQ ID NO:3 of PCT US99/20730.

I need SEQ ID NO:1 to be at least 93% identical with SEQ ID NO:3. I also need SEQ ID NO:2 to be at least 80% identical with SEQ ID NO:3.

NO 60/097,960

Is this possible? Thank You!

Terra Cotta Gibbs, Ph.D. Art Unit 1635 CM1, 12A12 703-306-3221 Run 59 12 2

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## SEARCH REQUEST FORM

### Scientific and Technical Information Center

Requester's Full Name:		l:x	ammer = :	<u>.</u>	Date:		
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Mail Box and Bldg/Room Location:		_ Results	Fonnat Prefen	red (circle):	PAPER	DISK	E-MAII
If more than one search is submitte	ed, please p	rioritize s	earches in or	der of ne	ed.	****	*****
Please provide a detailed statement of the seal include the elected species or structures, keyw utility of the invention. Define any terms that known. Please attach a copy of the cover sheet	vords, synonyn i may ḥave a sr	ns, acronyms pecial meanir	, and registry nu- ig. Give example	mbers, and c	ombine wi	th the co	ncept or
Title of Invention:							
Inventors (please provide full names):						<u> </u>	·
Earliest Priority Filing Date:							
*For Sequence Searches Only* Please include a appropriate serial number.	ill pertinent info	ormation (pare	ent, child, division	al, or issued p	atent numb	ers) alonį	g with the
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Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
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Contact: Sharing Zabo, William Nierman, Mark Adams
Department of Enkaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: bbedig: ozg
Clones are derived from the human BAC library RPCI-11. For BAC
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library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html. Seq primer: T?
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RPCI11 Human Male BAC_Library"
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Mus musculus
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                                                                                                                                                                                                                                             /mol_type="genomic_DNA"
/db_xref="GDB:7590285"
/db_xref="taxon:9606"
/clone="RPCI-11-236B22"
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Mus musculus (house mouse)

VERSION KEYWORDS SOURCE ORGANISM

Mus musculus

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Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Instrain Schaodtigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bozpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.igr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 105 row: P column: 3
Seg primer: SP6
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/clone_lib="RPCI-23"
/clone_lib="RPCI-23"
/clone_lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney_and/or
brain genomic DNA was isolated and partially disested
with a combination of ECORI and ECORI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
"As close 143 t
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Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                 Zhao,S., Nierman,W., Feldblyum,T., Malek,J.,
,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K
and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                   Mouse BAC End Sequences from Library RPCI-23
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/organism="Mus musculus"
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Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                          Mus musculus (house mouse)
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BY091041.1 GI:26204320
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Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genomicsohri.co.jp
HRI human CDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; CDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
               374 GGAATGAAATTCACCTGCTCTGAATTGGCCACTGGTGGGGGCAGGGGTGTGGCTTGGC
                                                                 1947 TTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATATAAGCTGACCGGTGTGGAGG
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AU139209 PLACE1 Homo sapiens CDNA clone PLACE1010155 5', mRNA
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Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Fax: 81-438-52-3975
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11.6%; Score 241; DB 9; 1
Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 241; Conservative 0; Mismatches 0;
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| Organism="Homo sapiens"
| mol_type="mRNA"
| db xref="taxon:9606"
| clone="PLACE1010155"
| fissue type="placenta"
| clone lib="PLACE1"
| note="Vector: pME18SFL3"
| a 154 c 181 g 156 t
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HRI human cDNA project
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Homo sapiens
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                                                                                                                                                                                                                                                                                        sequence.
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Namadalis butnerla; kodentia; Sciurognachi; Muridae; Murinae; Musiacot in Dases i to 371)

Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanakai, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Quackenbush, J., Saito, R., Bult, C., Hune, D.A., Golobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hune, D.A., Betalov, S., Beisel, K.W., Blake, J.J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Kanai, A., Kawai, H., Necther, C.F., Forrest, A., Frazer, K.S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Kanai, A., Kawai, H., Wackawa, N., Jackson, I. J., Jarvis, B. D., Kanai, A., Kawai, H., Warchionni, L., Mcherski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P. A., Maltais, I., Marchionni, L., Mcherski, R. B., Lyons, P. A., Maltais, I., Schneider, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Redd, J.U., Qi, D., Ramachandran, S., Ravasi, T., Redd, J.U., Qi, D., Ramachandran, S., Ravasi, T., Redd, J.U., Qi, D., Ramachanda, K., Sultana, R., Takenaka, Y., Taylor, M., Sakamura, M., Sakazune, N., Vang, I., Yang, I., Yang, I., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishia, K., Satoki, D., Malaysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Antalysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
BY091041
BY091041 RIKEN full-length enriched, 10 days neonate heart Mus
musculus cDNA clone K630084E21 5', mRNA sequence.
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URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishli,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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TITLE
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1 (bases 1 to 353)
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Salto,R., Suzuki,H., Yamanaka,I., Kiyosawa,H.,
Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C.,
Gojobori,T. Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A.,
Ouackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S.,
Beisel,K.W., Blade,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani, L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library, Genome Res. 11 (2), 281-289 (2001) CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Science Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119
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/tissue_type="heart"
/dev_stage="10 days neonate"
/clone_lib="RIKEN full-length enriched, 10 days neonate
heart"
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                                                                                                                                                                                             prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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81.3%; Pred. No. 0.012;
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/mol_type="mRNA"
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Computational Analysis of Pull-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
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Computer-based methods for the mouse full-length cDNA
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encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Science Laboratory in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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URL:http://genome.gsc.riken.go.jp/
Alzawa,K., Akimura,T., Arakwa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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/clone_lib="RIKEN full-length enriched, 10 days neonate
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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Fax: 81-45-503-9216
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/clone="INAGE:30376302"
/tissue_type="White Matter"
/dev_stage="Unknown"
/dev_stage="Unknown"
/lab_host="Dh10B-170 A ( T1 and T5 phage resistances)"
/clone_lib="NIH MGC_181"
/clone_lib="Vetor: pCNV-SPORT6.1; Site_1: Not1; Site_2: ECORV (Actes="Vetor: pCNV-SPORT6.1; Site_1: Not1; Site_2: ECORV (Actes yellow); Library is oligo-dT primed and directionally cloned (ECORV site is destroyed upon cloning). Average insert size 1.42 kb. Library was constructed by (Invitrogen). Note: this is a NIH MGC_Library."
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11 MH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished
                                                                                                                                                                                                                                                                                                  1096 CCTGCCATTGCTAATATCTGGTCTCATTTTTBTCATATATATATATATTTGTGGTAG
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Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM38 row: I column: 07
High quality sequence stop: 638.
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AGENCOURT 14096429 NIH_MGC_181 Homo sapiens CDNA clone
IMAGE:30376302 5′, mRNA sequence.
                                           Length 343;
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Pred. No. 5.5e+02;
0; Mismatches 44; Indels 0
                                                                               Indels
                                                                                   54;
                                           DB 28;
                                         Score 98.6; DB 28
Pred. No. 9.6e+02;
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Matches 125; Conservative
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  library availability passe contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
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                                   1748 GACAAATAGGATGACTTGCATTGCTGAGCGATGTGATCACCACCAAAGGAATGGCCCTCT
                                                             2 GATACGTGGGATGACTCGCATTGCTGAGCGTGTGGTCACTGCCAAAGGAATGACCTCT
                                                                                                                                                                                                                          117 CTTCCCAGACACTAAGTCTGGAATGAAATTCACCTGCCTCTGAATTGGCCACTGGTGGG
                                                                                                                                                                                                                                                                                                                                              Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
   Gaps
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   Indels
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Zhao,S., Adams,M.D., Nierman,W., Malek,J.,
 73;
 Mismatches
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LIANL at:

www-bio.llnl.gov/bbrp/image/image.thml
Insert Length: 841 Std Brror: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 408.
                                                                                                                                                                            AA494075 412 bp mRNA linear EST 19-AUG-1997 ng61c08.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:939278 similar to contains Alu repetitive element;, mRNA sequence.
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//note="Vector: pAMPl0; mRNA made from liposarcoma, cDNA
/note="Vector: pampl0; mRNA made from liposarcoma, cDNA
made by oligo-dT priming. Non- directionally cloned.
Size-selected on agarose gel, average insert size 600 bp.
Reference: Krizman et al. (1996) Cancer Research
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Pred. No. 1.4e+03;
0; Mismatches 40;
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/lab_host="DH108"
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/db_xref="taxon:9606"
/clone="IMAGE:939278"
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                           1314 TTTTGAAGTAAA 1325
                                                                    471 TTGCAACATAAA 482
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                                                                                                                                                                                                                                                                                                               AQ207760 502 bp DNA linear GSS 18-SEP-1998 HS_3026_B1_G10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026 Col=19 Row=N, genomic survey
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                           523
                                                                       318 AAGATTAGCATGGACTCTGTGCAAGAATGACACACAAATTTGTGAAACATTCCATATATT 377
                                                                                                              522 AAGATTAGCATGGCCCCTGCGCAAGGATGACACGCAAATTCGTGAAGCGTTCCATATTTA 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
1135 TATATATATAGTATTTGTGGTAGAGGGATTTTTGCCATGTTGCCCAGGCTAGTATTGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          351 TCCTGAGCTCAAGCAGTCTGCCTCAGCCTCGCAAAGTGCTGGGATTACAGGCATAA
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Proc. Natl. Acad. Scl. U.S.A. 96 (17), 9739-9744 (1999)
99380589
                                                                                                                                                              378 AAAAATAAATAAATAAAGAGAAAAAGGAAAAAATTAAAAAGAAAATA 426
                                                                                                                                                                                                     Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Email: jwallace@u.washington.edu
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ilarity 71.9%; Pred. No. 1.1e+03;
Conservative 0; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3026 Col=19 Row=N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Mahairas GG, Wallace JC, Hood L
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Location/Qualifiers
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Class: BAC ends
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Matches 138; Conserv
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HS 3026 E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /done lib="Soares NFL T GBC S1"
/robe="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI CGAP GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization teaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.MA-G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homosapiens, Similar to hypothetical protein FLJ20489, clone BC038630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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ol51f11.sl Soares NFL T GBC S1 Homo sapiens cDNA clone
IMAGE:1527021 3' Similar to SW:TSG6 HUMAN P98066 TUMOR NECROSIS
FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR ;contains Alu repetitive
                                                                                                                                                                        Bukaryora, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 464)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL , contact the
This Consortium (infc@image.llnl.gov) for further information.
Insert Length: 417 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 345.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGS:1527021"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
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96
                                                             element;, mRNA sequence.
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AA917468.1 GI:3057358
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Homo sapiens
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BC038630
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AI039619 315 bp mRNA linear EST 30-JUN-1998 ox28f05.x1 Soares total fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1657665 3' Bimilar to WP:T20D3.3 CE03672 ;, mRNA sequence.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 2772)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 315)
                                                                                                                                                        Direct Submission
Submitted (15-007-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 73 Row: i Column: 4 This clone has the following problem: retained intron. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shira
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
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/clone_lib="NIH MGC_95"
/lab_host="DH10B"
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623 c 602 g 865 t
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5263792"
                                                                                                                                                                                                                                                                                                                                                                                                  Contact: MGC help desk
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                                                                                                              Strausberg, R
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases 1 to 369)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Matsukuma,A., deliveire,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                         Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 296.
Location/Qualifiers
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Pred. No. 1.9e+03;
0; Mismatches 47; Indels (
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Unpublished
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                       1. .315
/organism="Homo sapiens"
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BF738217.1 GI:12064893
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/organism="Homo sapiens"
/mcl_type="mRNA"
/db_trefe".taxon:9606"
/dev_stage="Adult"
/clone_lib="KT0033"
/note="forgan: bladder tumor; Vector: puc18; Site_1: Smal;
/note="forgan: bladder tumor; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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1 (bases 1 to 464)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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                                                                                                                                                          Fax: +55-11-270701
Email: asimpson@ludwig.org.br
This asquence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-KT0033-
151200-572-f07&t3=2000-12-15&t4=1)
Seg primer: puc 18 forward
High quality sequence start: 15
High quality sequence stop: 369.
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MR1-HN0070-151200-003-h04 HN0070 Homo sapiens cDNA, mRNA sequence.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Pred. No. 1.8e+03;
0; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 g
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ilarity 67.3%;
Conservative (
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                                                                                                                                  rel: +55-11-2704922
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymerase and 74 polymerase ared with 74 DNA polymerase and 74 polymerlectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarces gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil/473114) gbl/AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into capacity competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 AATAGGAGCTATACAAAGAAGATTAGCATGGACTCTGTGCAAGAATGACACACAAATTTG
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plasmid inserts
Unpublished
Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S.
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                        Insert Length: 10000 Std Brror: 0 Plate: 0065 row: G column: 12 Seq primer: CACACAGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 723. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0065G12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
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/ Mol type="mRNA"

/ db_xref="waxna:9606"
/ dev_stage="Adult"
/ clone lib="HN0070"
/ note="Organ: head normal; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES POR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
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Fax: +55-11-2707001

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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR1&t2=MR1-HN0070-151200-003-h04&t3=2000-12-15&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 17

High quality sequence start: 17

High quality sequence stop: 464.
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 723)
Eunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Elam, M., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
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                                                                                                                                  Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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67.9%; Pred. No. 1.6e+03;
tive 1; Mismatches 66;
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                                                                        Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
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AUTHORS
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Sequence 3, Application US/09740041
Patent No. 6562593
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLOONO1
CURRENT APPLICATION NUMBER: US/09/740,041
CURRENT FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: MacKenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Liston, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Tsang, Benjamin K
APPLICANT: Trang, Benjamin K
APPLICANT: Trang, Benjamin K
APPLICANT: Trang, Benjamin K
APPLICANT: Dratt, Christine
TITLE OF INVENTION: DRESCTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
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US-09-755-934A-3
US-09-76-302-3
US-09-76-302-3
US-09-345-882-1
US-09-740-04-3
US-09-740-04-3
US-09-740-05-4
US-09-740-35-4
US-09-106-375-4
US-09-106-375-4
US-09-118-512-3
US-09-1211-10
US-09-128-155-16
US-09-128-155-16
US-09-128-155-16
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US-09-784-316-3
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; Sequence 5, Application US/09212971B
; Patent No. 6107041
; GENERAL INFORMATION:
4.1 246240
4.0 43950
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es 118; Conserv
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US-09-740-041-3
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LENGTH: 66804
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Sequence 200,
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Sequence 35
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(cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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Compugen Ltd.
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US-09-212-971-5
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US-09-918-197-3
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US-09-641-638-651
US-09-729-995-3
US-09-729-74-7
US-09-739-739-7
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                                                                                                                                                                                                                                                                        569978 segs, 220691566 residues
               GenCore version
Copyright (c) 1993 - 2003
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Listing first 45 summaries
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1194

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APPLICANT: MacKenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Liston, Peter
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Brack, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: UNBERS: 07891/009003
TITLE OF INVENTION: 08/09/617,053A
CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ 1D NOS: 17
SOFTWARE FASTESEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1195 TCCTAAGCT-AAGCAATCTTCCTGTCTCTGCCTCCCAAAATGTTGGGATTACAGGTGTAA 1253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 89.4; DB 3;
Pred. No. 7.2e-13;
0; Mismatches 46;
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; OTHER INFORMATION: n can be any nucleotide US-09-617-053A-5
                                                                          NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER:
REPERENCE/DOCKET NUMBER: 07891/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 5, Application US/09617053A; Patent No. 6300492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 73.1%;
Matches 128; Conservative
                            FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bieker-Brady, Krist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Korneluk, Robert G
                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 6669 base pairs
                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: cDNA US-08-800-929A-5
                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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LENGTH: 6669
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4.3%; Score 89.4; DB 3; Length 6669;
Best Local Similarity 73.1%; Pred. No. 7.2e-13;
Matches 128; Conservative 0; Mismatches 46; Indels 1
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
TITLE OF INVENTION: DISEASE

FILE REFERENCE: 07891/009002

CURRENT APPLICATION NUMBER: US/09/212,971B

CURRENT FILING DATE: 1998-12-16

EARLIER APPLICATION NUMBER: 60/017,354

EARLIER FILING DATE: 1996-04-26

EARLIER FILING DATE: 1996-11-14

EARLIER FILING DATE: 1996-11-14

EARLIER FILING DATE: 1997-02-13

NUMBER OF SEQ ID NOS: 17

SOFTWARE: FRIENG DATE: 1997-02-13

NUMBER OF SEQ ID NOS: 17

SOFTWARE: FASISEQ for Windows Version 4.0

SENGTH: 6669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: variation
; LOCATION: (3677)...(3951)
... OTHER INFORMATION: n can be any nucleotide
US-09-212-911-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997
CLASSIFICATION: 424
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APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Teang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MC
TITLE OF INVENTION: IMPS AND NAIP FO
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FILING DATE: 14-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08800929A Patent No. 6133437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clark & Elbing LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 Federal Stree
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & E
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
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78.1%;
  Best Local Similarity 78.1
Matches 118; Conservative
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Best Local Similarity
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ORGANISM: Human
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US-09-641-638-36
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Patent No. 6492156

GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CLOO1306
CURRENT APPLICATION NUMBER: US/09/984,890

CURRENT FILING DATE: 2001-10-31

NUMBER OF SEQ ID NOS: 4

SOFTMARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09813817
Patent No. 6340583
GENERAL INFORMATION:
APPLICANT: YAM, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO1178
CURRENT APPLICATION NUMBER: US/09/813,817
CURRENT FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 4
                                                                      1290 TCCTGACCTCAAGTGATCCACTTGTCTTGGCCTCCCAAAATGCTGGGATTACAGGCGTGA 1349
1230 TAATTTTTGTATTTTTAGTAGAGGGTTTCACCATTTTGGCCAGGCTGGTTTTGAAC 1289
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                                           1195 TCCTAAGCT-AAGCAATCTTCCTGTCTCTGCCTCCCAAAATGTTGGGATTACAGGTGTAA
                                                                                                                             1254 GCCACTGCACCCGGCTGATAGCTGGTTTCATTTACTCTATTTCTTGACCACTCTG 1308
                                                                                                                                                                        1350 GCCACTGCACCAGGCAGAGGCCTCTGTTTTTATCTCTTTTTGGCCTCTACAGTG 1404
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4.3%; Score 89.4; DB 4; Length 75395;
Best Local Similarity 72.1%; Pred. No. 1.8e-12;
Matches 129; Conservative 1; Mismatches 48; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3
LENGTH: 59065
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (1)...(75395)
; OTHER INFORMATION: n = A,T,C or
US-09-984-890-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature LOCATION: (1)...(75395)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 3
LENGTH: 75395
                                                                                                                                                                                                                                                               US-09-984-890-3
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4.2%; Score 87.8; DB 4; Length 59065;

Query Match

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Sequence 3, Application US/09978197

Sequence 3, Application US/09978197

Patent No. 6403153

GENERAL INFORMATION:

APPLICANT: VAN, Chunhua et al.

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

FILE REFERENCE: CLOO1178DIV

CURRENT FILING DATE: 2001-10-17

PRIOR FILING DATE: 2001-10-17

PRIOR FILING DATE: 2001-03-22

NUMBER OF SEQ ID NOS: 4

SEQ ID NO 3

LENGTH: 59065
                                                                                                                                                                                                                              11864 TCCTGACCTCAAGTGATCCACCTGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGTGTGA 11923
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Patent No. 6432648
GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
APPLICANT: Chuma
                                                        1;
                                                                                                                                                         1135 TATATATAGTATTTGTGGTAGAGATGGGATTTTGCCATGTTGCCCAGGCTAGTATTGAAC 1194
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                                                        Gaps
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Pred. No. 4.2e-12;
0; Mismatches 32; Indels
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Pred. No. 4.2e-12;
0; Mismatches 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCACTGCACCCGGCTGATAGCTGGTTTCAT 1284
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PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.2%;
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LOCATION: 1123..3123
OTHER INFORMATION: 5'regulatory region NAME/KEY: exon
LOCATION: 3124..3297
OTHER INFORMATION: exon 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: exon
LOCATION: 7379..7522
OTHER INFORMATION: exon 7
NAME/KEY: exon 7
LOCATION: 8645..8854
OTHER INFORMATION: exon 8
                                                                                                                                                                                                                                                                                                                                                                                                                                   OCHER INFORMATION: exon 5
                                                                                                                                                                                                                                                     OCATION: 3871..4072
THER INFORMATION: exon 2
                                                                                                                                                                                                                                                                                                                        JOCATION: 5552..5633
THER INFORMATION: exon 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OCATION: 6349..6509
THER INFORMATION: exon 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION: exon 9
                                                                                                                                                                                                                                                                                                                                                                                     JOCATION: 5758..5880
STHER INFORMATION: exon
                                                                                           NAME/KEY: misc feature
                                                  ORGANISM: Homo sapiens
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1176 GCCCAGGCTAGTATTGAACTCCTAAGCT-AAGCAATCTTCCTGTCTCTGCCTCCCAAAAT 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
                                                                                                                                                                                                                                          NAME/KEY: allele

LOCATION: 478

LOCATION: 478

OTHER INPORMATION: 10-349-47: polymorphic base C or T
NAME/KEY: misc_binding

LOCATION: 458...47

OTHER INPORMATION: 10-349-47.misl, potential

NAME/KEY: misc_binding

LOCATION: 479...498

OTHER INFORMATION: 10-349-47.mis2, potential complement

NAME/KEY: primer_bind

OTHER INFORMATION: upstream amplification primer

NAME/KEY: primer_bind

OTHER INFORMATION: downstream amplification primer

NAME/KEY: misc_binding

LOCATION: 459...66...490

LOCATION: 466...490

COTHER INFORMATION: 10-349-47 potential probe

US-09-641-638-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 956;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 86.8; DB 4;
Pred. No. 1.5e-12;
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4.2%; Score 86.8; D
Best Local Similarity 76.6%; Pred. No. 1.5e
Matches 118; Conservative 1; Mismatches
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR PLING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent.pm
SEQ ID NO 36
LENGTH: 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-641-638-651, Application US/09641638; Sequence 651, Application US/09641638; Patent No. 6432648; GENEAL INFORMATION: APPLICANT: Blumenfeld, Marta; APPLICANT: Bougueleret, Lydie
                                                                                                                                                                                                         ORGANISM: Homo Sapiens
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: variable motif ATTTA or TTTTTT
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THER INFORMATION: 10-511-337 : insertion of T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : deletion of C
                                                                                                                                                                                                                                                                                                  OCATION: 17555..20674
OTHER INFORMATION: 3'regulatory region
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1128
OTHER INFORMATION: 10-508-191 :
NAME/KEY: allele
LOCATION: 1182
OTHER INFORMATION: 10-508-245 :
NAME/KEY: allele
LOCATION: 1559
OTHER INFORMATION: 10-509-284 :
NAME/KEY: allele
LOCATION: 1570
OTHER INFORMATION: 10-509-295 :
NAME/KEY: allele
LOCATION: 1827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION: 10-510-173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-511-62
                                                     ION: 13308..13429
INFORMATION: exon 11
                                                                                                                    OCATION: 16567...16667
THER INFORMATION: exon 12
PAME/KEY: exon
                                                                                                                                                                              OCATION: 16775..16945
WTHER INFORMATION: exon 13
OCATION: 12854..13023
THER INFORMATION: exon 10
                                                                                                                                                                                                                                                            INFORMATION: exon 14
                                                                                                                                                                                                                                                                             AME/KEY: misc feature OCATION: 17555.20674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
                                       AME/KEY:
                                                                                                 AME/KEY:
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GENERAL INVENDATION:

APPLICANT: Bougueleret, Lydie

APPLICANT: Bougueleret, Lydie

APPLICANT: Chumakov, Ilya

TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING

TITLE OF INVENTION: GENEST: 08/09/641,638

TITLE OF INVENTION: GENEST: 08/00-08-16

CURRENT FILING DATE: 2000-02-11

CURRENT FILING DATE: 1000-02-11

PRIOR FILING DATE: 1999-05-07

PRIOR APPLICATION NUMBER: US 60/133,200

PRIOR APPLICATION NUMBER: US 60/133,200

PRIOR FILING DATE: 1999-03-23

PRIOR FILING DATE: 1999-02-12

NUMBER OF SEQ ID NOS: 1304

SEQ ID NO 651

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LOCATION: 2341
OTHER INFORMATION: 10-512-36 : polymorphic base G or
                                                                                                                                                                                                                                                                                                                                          : polymorphic base A or
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                                                                   : polymorphic base A
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                                                                                                                                                                                                                                                                                                                                                                                                 : deletion of C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 4170

CTHER INFORMATION: 10-343-339 :
NAME/KEY: allele
LOCATION: 5903

OTHER INFORMATION: 10-346-23 :
NAME/KEY: allele
LOCATION: 6019

OTHER INFORMATION: 10-346-141 :
                              NAME/KEY: allele
LOCATION: 2623
OTHER INFORMATION: 10-512-318
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: allele
LOCATION: 6375
NOTHER INFORMATION: 10-347-111
LOCATION: 6429
                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: allele
LOCATION: 4062
OTHER INFORMATION: 10-343-231
                                                                                                                                                                                                              LOCATION: 2934
OTHER INFORMATION: 10-513-352
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 4088
OTHER INFORMATION: 12-206-366
NAME/KEY: allele
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OTHER INFORMATION: 10-343-278
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LOCATION: 6183
OTHER INFORMATION: 10-346-305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: allele
LOCATION: 6484
OTHER INFORMATION: 10-347-220
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LOCATION: 6611
OTHER INFORMATION: 10-347-348
NAME/KEY: allele
                                                                                                       LOCATION: 2832
OTHER INFORMATION: 10-513-250
                                                                                                                                                           LOCATION: 2844
OTHER INFORMATION: 10-513-262
                                                                                                                                                                                                                                                                     LOCATION: 2947
OTHER INFORMATION: 10-513-365
                                                                                                                                                                                                                                                                                                        NAME/KEY: allele
LOCATION: 3802
OTHER INFORMATION: 12-206-81
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OTHER INFORMATION: 10-347-271
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OTHER INFORMATION: 10-348-391
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OTHER INFORMATION: 10-347-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: allele
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LOCATION: 6141
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LOCATION: 6467
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LOCATION: 8608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1176 GCCCAGGCTAGTATTGAACTCCTAAGCT-AAGCAATCTTCCTGTCTCTGCCTCCCAAAAT 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8139 GCCACCATGTGGGCCTGGCTAATTTTTGTATTTTTTTTGTAGAGATGGGGTTTTCGCCATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1116 GTCTCATTTTTBTCATATATATATATATATTTGTGGTAGAGATGGGATTTTTGCCATGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 86.8; DB 4; Length 20674;
Pred. No. 5e-12;
1; Mismatches 34; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 99500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Donna T. Ward
APPLICANT: Addrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF RECQL2 EXPRESSION
FILE REFERENCE: RIS-0207
CURRENT APPLICATION UNBER: US/09/798,096
CURRENT FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 89
                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: 10-350-72 : polymorphic base C or T NAME/KEY: allele  
LOCATION: 12429  
COTHER INFORMATION: 10-350-332 : polymorphic base C or T NAME/KEY: allele  
LOCATION: 13341  
COTHER INFORMATION: 10-507-170 : polymorphic base A or G NAME/KEY: allele  
LOCATION: 13492  
COTHER INFORMATION: 10-507-321 : polymorphic base A or C NAME/KEY: allele  
LOCATION: 13524  
LOCATION: 13524  
COTHER INFORMATION: 10-507-353 : polymorphic base C or T NAME/KEY: allele
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                                                                                                                                                                                    : polymorphic base G or T
                                                                                                                                                                                                                                                : polymorphic base C or T
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                                                            : polymorphic base G or
: polymorphic base A or
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Pred. No. 1.3e-11;
0; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1235 GTTGGGATTACAGGTGTAAGCCACTGCACCCGGC 1268
                                                                                                                        : deletion of CTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/09798096; Patent No. 6399378; GENERAL INFORMATION:
                                                                                                                                                                                                                                                OTHER INFORMATION: 10-349-368
NAME/KEY: allele
LOCATION: 12171
                                                                                                                    OTHER INFORMATION: 10-349-216
NAME/KEX: allele
LOCATION: 8785
OTHER INFORMATION: 10-349-224
                                                              10-349-142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 76.6%;
Matches 118; Conservative
INFORMATION: 10-349-97
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Best Local Similarity 75.5
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                          OTHER INFORMATION:
NAME/KEY: allele
                                                                                                                                                                                                       NAME/KEY: allele
LOCATION: 8926
                     WAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: allele
LOCATION: 13535
                                                                                                LOCATION: 8777
OTHER INFORMAT
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LENGTH: 99500
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US-09-798-096-10
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TYPE: DNA ORGANISM: Homo sapiens
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US-09-657-474-7/c
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32693 ATTITITITITITITITITITITITITICACGUITICACCATGITIGGCCAGGCTGGTCTCGAACT 32752
                                                                                                                     32753 CCTGACCTCAAGCATTCCACCTGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAG 32812
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                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: WO. 94-72-200
GENERAL INCORMATION:
APPLICANT: WEI, Ming-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID WOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CLOGO904
CURRENT APPLICATION NUMBER: US/09/729,995
CURRENT PILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3:
LENGTH: 29629
                                                                          CCTAAGCT-AAGCAATCTTCCTGTCTCTGCCTCCCAAAATGTTGGGATTACAGGTGTAAG 1254
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US-09-266-992-7/c

Sequence 7, Application US/09268992

Patent No. 6342351

GENERAL INFORMATION:
APPLICANT: Chen, H.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS;
TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS;
TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS;
CURRENT APPLICATION NUMBER: US/09/268,992

CURRENT FILING DATE: 1999-01-25

EARLIER APPLICATION NUMBER: 60/106,056

EARLIER FILING DATE: 1998-10-28

EARLIER FILING DATE: 1998-01-65

EARLIER FILING DATE: 1998-03-16

NUMBER OF SEQ ID NOS: 84

SOFTWARE: FEASTER FILING DATE: 1998-03-16

NUMBER OF SEQ ID NOS: 84

SEQ ID NO 7

LEANTH OF THE SECOND NOS: 84
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Pred. No. 9.2e-12;
0; Mismatches 30; Indels
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                                                                                                                                                                      1255 CCACTGCACCCGGCTGATAGCTGGTTTCATTTACTCTAT 1293
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illarity 77.6%;
Conservative
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Best Local Similarity
Matches 104; Conserv
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; ORGANISM: Human
US-09-729-995-3
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Sequence 7, Application US/09657474

Patent No. 6399762

GENERAL INFORMATION:
APPLICANT: Freimer, N.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
CURRENT APPLICATION NUMBER: US/09/657,474

CURRENT APPLICATION NUMBER: US/09/657,474

PRIOR APPLICATION NUMBER: 09/266,992
PRIOR FILING DATE: 1999-03-16

PRIOR FILING DATE: 1999-03-16

PRIOR APPLICATION NUMBER: 06/106,056

PRIOR PILING DATE: 1998-10-28

PRIOR PILING DATE: 1998-04-05

PRIOR PILING DATE: 1998-03-16

PRIOR PILING DATE: 1998-03-16

NUMBER OF SEQ ID NOS: 84

SOFTWARE: FRACESQ for Windows Version 3.0

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                                                                                                                                                            Score 85.8; DB 4; Length 72604;
Pred. No. 1.5e-11;
0; Mismatches 42; Indels 0;
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4.1%; Score 85.8; DB 4;
Best Local Similarity 72.5%; Pred. No. 1.5e-11;
Matches 111; Conservative 0; Mismatches 42;
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OTHER INFORMATION: n=a, c, g,
NAME/KEY: modified base
DOCATION: all n positions
OTHER INFORMATION: n=a, c, g,
US-09-268-92-7
                                                                                                                                                               4.1%;
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                                                                                                               Sequence 3, Application US/09984890

Sequence 3, Application US/09984890

Batent NO. 6492156

GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MCLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO01306

CURRENT APPLICATION NUMBER: US/09/984,890

CURRENT FILING DATE: 2001-10-31

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 6492153
GENERAL INFORMATION:
APPLICANT: ABU-THREIDEH, Jane et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TILLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TILLE REFERENCE: CL001043
CURRENT APPLICATION NUMBER: US/09/759,359A
CURRENT FILING DATE: 2001-01-16
NUMBER: OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 90541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.1%; Score 85.8; DB 4; Length 75395; 78.6%; Pred. No. 1.5e-11; Live 1; Mismatches 29; Indels 1;
57460 CCACCACACCCGGCTGTATGAAGCATGTTTTA 57428
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LOCATION: (1)...(75395)
OTHER INFORMATION: n = A,T,C or G
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Matches 114; Conservative
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Matches 117; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Human
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LENGTH: 75395
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Search completed: November 14, 2003, 06:49:03 Job time : 120.926 secs

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APPLICANT: BENDIT, Patrick
APPLICANT: SCHWARTZ, Bertrand
APPLICANT: BRANBLEC, Didder
APPLICANT: BRANBLEC, Didder
APPLICANT: BRANBLEC, Didder
TITLE OF INVENTION: THEM AND USES THEREOF
TITLE OF INVENTION: THEM AND USES THEREOF
FILE REFERENCE: 03806.0530-00000
CURRENT APPLICATION NUMBER: US/10/005,337A
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/251,582
PRIOR FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 5
SOFTWARE PATENTING DATE: 2.000-12-07
SEQ ID NOS: 5
SEQ ID NO 2
LENGTH: 2074
                 Sequence 3, Appli
Sequence 27383, A
Sequence 27383, A
Sequence 27384, A
Sequence 27384, A
Sequence 27384, A
Sequence 27384, A
Sequence 2713, Appl
Sequence 2713, Appl
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                                   US-09-918-995-35181

US-10-027-632-27383

US-10-027-632-27383

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US-10-027-632-27384

US-09-782-3784-17

US-09-782-3784-17

US-09-782-3784-17

US-10-027-632-113259

US-10-027-632-113259

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US-10-027-632-102687

US-10-027-632-102688
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US-10-027-632-110575
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100.0%; Pred. No. 0;
iive 0; Mismatches
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                                            Query Match
Best Local Similarity 100.
Matches 2074; Conservative
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ORGANISM: Homo sapiens
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Sequence 217, App
Sequence 1029, Ap
Sequence 1029, Ap
Sequence 1029, Ap
Sequence 33, Appl
Sequence 33, Appl
Sequence 3933, Ap
Sequence 95562, A
Sequence 95562, A
Sequence 95562, A
Sequence 95562, A
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Sequence 182, App
Sequence 158, App
                                                                                                                                         ; Search time 613.964 Seconds (without alignments) 11040.154 Million cell updates/sec
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Sequence 1, Appli
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1: \cgn2 \( \) \cgn2 \( \
                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-262-552-33
US-09-764-877-3933
US-10-027-632-95562
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US-10-005-337A-1

US-09-974-298-182

US-10-240-965-158

US-10-252-157-421

US-09-923-876-5218

US-09-923-876-5218

US-09-764-860-1029
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                                                                                                                                           November 14, 2003, 03:51:42
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Maximum Match 100%
Listing first 45 summaries
                                                                                                 nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                IDENTITY NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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2074
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Match Length
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1929 GCGGGAGTGTTACTTCGGTTCCCAGGTTGGAAGATTATCTCACCCGGCCCCCAGCTATATA
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OTHER INFORMATION: Incyte ID No. US20020156263A1 332919.4
                     APPLICANT: Chen, Hoei-Mei
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILE REFERENCE: PA-0037 P
CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,331
PRIOR PILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL PROGram
SEQ ID NO 182
LENGTH: 1889
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COCATION: 1882
I CHER INFORMATION: a, t, c, g, or other
US-09-974-298-182
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Best Local Similarity 99.3
Matches 145; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                          22; Gaps
                                                                                                                                                                Length 2358;
                                                                                                                                                              Score 367.8; DB 14; Length
Pred. No. 1.2e-83;
0; Mismatches 162; Indels
                                                                                                                                                              17.78;
76.48;
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                           Query Match
Best Local Similarity 76.43
Matches 597; Conservative
                                                           LENGTH: 2358
TYPE: DNA
ORGANISM: Mus musculus
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Length 1889;

DB 10;

Score 144.4; DB 10 Pred. No. 2.6e-26; 0; Mismatches 1,

7.0%;

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1; Indels

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APPLICANT: MINITA, Thomas
APPLICANT: TAI, Julie
TITLE OF INVENTION GENES EXPRESSED IN FOAM CELL DIFFERENTIATION
FILE REFERENCE: PA-0025 PCT
CURRENT APPLICATION NUMBER: US/10/240,965
PRIOR APPLICATION NUMBER: 60/195,106
PRIOR APPLICATION NUMBER: 60/195,106
PRIOR PILING DATE: 2000-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030165924A1 332919.4
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: LOCATION: 1655-1681, 1882

: OTHER INFORMATION: a, t, c, g, or other

US-10-240-965-158
Sequence 158, Application US/10240965
Publication No. US20030165924A1
GENERAL INFORMATION:
                                                                                 APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: SHIFFWN, DOV
APPLICANT: LAWN, Richard M.
APPLICANT: LAWN, Richard M.
APPLICANT: SELLHAMER, Jeffrey J.
APPLICANT: PORTER, GORDON J.
APPLICANT: MIKITA, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 276
SOFTWARE: PERL Program
SEQ ID NO 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
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Sequence 182, Application US/09974298 Patent No. US20020156263A1

RESULT 3 US-09-974-298-182

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CURRENT APPLICATION NUMBER: US/10/084,817
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Length 1889;
                                           1; Indels
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OTHER INFORMATION: Incyte ID No. US20030190640A1 332919.4
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APPLICANT: Faris, Mary
ITLE OF INVENTION: GENES EXPRESSED IN PROSTATE CANCER
FILE REFERENCE: PA-0027-1 US
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: 60/295,048
PRIOR APPLICATION NUMBER: 60/295,048
PRIOR APPLICATION NUMBER: 60/295,048
PRIOR FILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 501
SOFTWARE: PERL PROGRAM
SOFTWARE: PERL PROGRAM
LENGTH: 1889
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APPLICANT: Jed G. Nuchtern
APPLICANT: Jacon B. Plon
APPLICANT: Jason M. Shohet
TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
FILE REFERENCE: PA-0046 US
  DB 12;
    Score 144.4; DB 13
Pred. No. 2.6e-26;
0; Mismatches 1
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99.3%; Pred. No. 2.6e-26;
cive 0; Mismatches 1
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; NAME/KEY: unsure
; LOCATION: 1655-1681, 1882
; OTHER INFORMATION: a, t, c, g, or other
US-10-252-157-421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 217, Application US/10084817; Publication No. US20030119009A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             Sequence 421, Application US/10252157
Publication No. US20030190640A1
GENERAL INFORMATION:
                      99.3%;
  Query Match
Best Local Similarity 99.3
Matches 145; Conservative
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ORGANISM: Homo sapiens
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US-10-084-817-217
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US-10-252-157-421
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patent No. US200200139581

patent No. US200200139581

patent No. US200200139581

GENERAL INFORMATION:

APPLICANT: Lalgudi, Raghunath V.

APPLICANT: Kamigaki, Laura Y. (Ito)

APPLICANT: Sherman, Bradley K.

TITLE OF INVENTION: POLYNOLICEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING

FILE REFERENCE: PL.0012-1 CON

CURRENT FILING DATE: 2001-08-06

PRIOR FILING DATE: 1999-04-21

PRIOR FILING DATE: 1999-04-21

PRIOR FILING DATE: 1998-06-05

NUMBER OF SEQ ID NOS: 6332

SOFTWARE: PERL PROGRAM

SEQ ID NOS: 6332

SEQ ID NO 5218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1928 GGCGGGAGTGTTACTTCCGGTTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATAT 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1932 GGAGTGTTACTTCGGTTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGGGGGAGTGTTACTTCGGTTCCCAGGTTTGAAGATTATCTCACCGGGCCCCAGCTATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.8%; Score 141.4; DB 14; Length 1325; Best Local Similarity 99.3%; Pred. No. 1.3e-25; Matches 142; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.2%; Score 129.4; DB 9; Length 184; Best Local Similarity 95.3%; Pred. No. 4.6e-23; Matches 141; Conservative 0; Mismatches 6; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20020013958A1 700456617H1
                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030119009A1 183198CB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: unsure

LOCATION: 67, 74, 98, 106, 122, 129

OTHER INFORMATION: a, t, c, g, or other

US-09-923-876-5218
                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: a, t, c, g, or other US-10-084-817-217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2052 CATACAAGACTCCTTCAGCCAAC 2074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 caracaagacrecrreagecaae 143
CURRENT FILING DATE: 2002-02-
PRIOR APPLICATION UNMBER: 60/2:
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 365
SOFTWARE: PERL Program
SEQ ID NO 217
LENGTH: 1325
                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                          NAME/KEY: unsure LOCATION: 1258
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R PILING DATE: 2000-08-14

R APPLICATION NUMBER: 60/226,868

R APPLICATION NUMBER: 60/216,647

R FILING DATE: 2000-08-22

R APPLICATION NUMBER: 60/215,267

R FILING DATE: 2000-07-07

R FILING DATE: 2000-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R FILING DATE: 2000-12-08
R APPLICATION NUMBER: 60/251,868
RR APPLICATION NUMBER: 60/229,344
RR PILING DATE: 2000-09-01
R APPLICATION NUMBER: 60/234,997
R FILING DATE: 2000-09-25
RR FILING DATE: 2000-09-28
R FILING DATE: 2000-09-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R FILING DATE: 2000-09-21
R APPLICATION NUMBER: 60/234,223
R FILING DATE: 2000-09-21
R FILING DATE: 2000-08-30
R FILING DATE: 2000-08-30
R APPLICATION NUMBER: 60/224,518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R FILING DATE: 2000-08-14
R RAPLICATION NUMBER: 60/236,369
RR FILING DATE: 2000-09-29
R APPLICATION NUMBER: 60/224,519
R FILING DATE: 2000-08-14
R FILING DATE: 2000-08-14
R FILING DATE: 2000-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R FILING DATE: 2000-11-01
R APPLICATION NUMBER: 60/225,268
R FILING DATE: 2000-08-14
R APPLICATION NUMBER: 60/236,368
R FILING DATE: 2000-09-29
R APPLICATION NUMBER: 60/251,856
                                                                                                                                                                                                                                                                                                  PILING DATE: 2000-07-07
APPLICATION NUMBER: 60/225,270
FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/251,869
                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2000-12-08
APPLICATION WUMBER: 60/235,834
FILING DATE: 2000-09-27
APPLICATION NUMBER: 60/234,274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/241,809
FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/249,299
FILING DATE: 2000-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 2000-09-29
APPLICATION NUMBER: 60/241,785
FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/244,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2000-09-01
APPLICATION NUMBER: 60/229,287
FILING DATE: 2000-09-01
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APPLICATION NUMBER: 60/229,345
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APPLICATION NUMBER: 60/231,413
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APPLICATION NUMBER: 60/236,370
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        PRILOR PR
1136 ATATATAGTATTTGTGGTAGAGATGGGATTTTGCCATGTTGCCCAGGCTAGTATTGAACT 1195
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                                                     61 AAGCTGNACCGGTNTGGAGGGCCCAGCAGGCCAACNCCAGGGANTCCTTCCACGACAG 120
                                                                                                                                                                                                                   US-00-764-860-1029/c

Sequence 1029, Application US/09764860

Sequence 1029, Application US/09764860

Sequence 1020 1032002004953A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC008

CURRENT APPLICATION NUMBER: US/09/764,860

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 1198

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1029

LUGTH: 6040
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCO08C1
CURRENT APPLICATION NUMBER: US/10/074,095
CURRENT FILING DATE: 2002-02-14
PRIOR PAPLICATION NUMBER: 09/764,860
PRIOR FILING DATE: 2001-01-17
PRIOR PAPLICATION NUMBER: 60/179,065
PRIOR PAPLICATION NUMBER: 60/179,065
PRIOR PELICATION NUMBER: 60/179,065
PRIOR PILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR PILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR PILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR PELING DATE: 2000-07-16
PRIOR PILING DATE: 2000-07-16
PRIOR PILING DATE: 2000-07-16
PRIOR PILING DATE: 2000-07-16
PRIOR FILING DATE: 2000-07-16
PRIOR FILING DATE: 2000-07-16
PRIOR FILING DATE: 2000-07-16
PRIOR FILING DATE: 2000-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.6%; Score 95.4; DB 9; Length 6040; ilarity 72.8%; Pred. No. 2.1e-13; Conservative 0; Mismatches 46; Indels 0
                                                                                                        2047 AAAAACATACAAGACTCCTTCAGCCAAC 2074
                                                                                                                                                             121 ANAAACATNCAAGACTCCTTCAGCCAAC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1029, Application US/10074095
Publication No. US20030077704A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-860-1029
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Best Local Similarity
Matches 123; Conserv
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PRIOR APPLICATION NUMBER: 60/236, 902
PRIOR APPLICATION NUMBER: 60/237, 040
PRIOR APPLICATION NUMBER: 60/239, 935
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/241, 787
PRIOR PILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/246, 734
PRIOR APPLICATION NUMBER: 60/246, 744
PRIOR APPLICATION NUMBER: 60/249, 216
PRIOR APPLICATION NUMBER: 60/226, 631
PRIOR PILING DATE: 2000-11-10
PRIOR PILING DATE: 2000-11-17
PRIOR PILING DATE: 2000-08-14
PRIOR PILING DATE: 2000-11-17
PRIOR PILING DATE: 2000-11-17
PRIOR PILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249, 209
PRIOR PILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249, 209
PRIOR PILING DATE: 2000-11-17
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09-09
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1196 CCTAAGCTAAGCAATCTTCCTGTCTTGCCTCCCAAAATGTTGGGATTACAGGTGTAAAGC 1255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1). (300000)
; OTHER INFORMATION: where n may be a or g or c or t/u, unknown or other
US-10-262-552-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1136 ATATATAGEATTTGTGGTAGAGATGGGATTTTGCCATGTTGCCCAGGCTAGTATTGAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 95.4; DB 14;
Pred. No. 2;1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; sequence 33, Application US/10262552; publication No. US20030125289A1; publication No. US20030125289A1; general INPORMATTON: GENERAL INPORMATTON: GENERAL TATEGIA, Marco TITLE OF INVENTION: MOONAN SYNDROME GENE; FILE REFERENCE: 2420/1J859-US1; CURRENT APPLICATION NUMBER: US/10/262,552; CURRENT FILING DATE: 2002-10-01; PRIOR FILING DATE: 2001-10-01; NUMBER OF SEQ ID NOS: 35; SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                             DR FILING DATE: 2000-09-14

DR APPLICATION NUMBER: 60/232,401

SR FILING DATE: 2000-09-14

DR APPLICATION NUMBER: 60/241,808

DR FILING DATE: 2000-10-20

R PELING DATE: 2000-10-20

R PILING DATE: 2000-10-20

R RILING DATE: 2000-10-20

R APPLICATION NUMBER: 60/241,786

R FILING DATE: 2000-10-20

R APPLICATION NUMBER: 60/241,786

R FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/232,080
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-14
PRIOR PELLORATION NUMBER: 60/233,064
PRIOR PELLING DATE: 2000-09-14
PRIOR PELLING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/233,397
PRIOR PILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232,397
PRIOR PILING DATE: 2000-09-14
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
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Best Local Similarity 72.8
Matches 123; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentl
SEQ ID NO 33
LENGTH: 300000
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US-10-262-552-33
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Score 94.8; DB 14; Length 300000; Pred. No. 3.3e-12;

Query Match Best Local Similarity

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30293 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTAGTAGAGATGGGGTTTTGCTATGTTG 30352
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                                                                                                                                                                                                                                                                                                                                                                                                 1117 TCTCATTTTTBTCATATATATATATATATTTTGTGGTAGAGATGGGATTTTGCCATGTTG 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1135 TATATATAGTATTTGTGGTAGAGATGGGATTTTTGCCATGTTGCCCAGGCTAGTATTGAAC 1194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: DOLYMORPHISMS in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR PAPLICATION NUMBER: US 60/193,483
PRIOR PAPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/195,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 12000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-08-09
SOFTWARE FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE FABRE FRANCE FARESO FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                   Length 32220;
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                                                                                                                                                                                                                                                                                   Score 93.2; DB 10; Length Pred. No. 2.2e-12; 1; Mismatches 30; Indels
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                                                                                                                 ; Sequence 95562, Application US/10027632; Publication No. US20030204075A9; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      4.5%;
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 79.2'
Matches 122; Conservative
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Matches 119; Conservative
                                                               TYPE: DNA
ORGANISM: Homo sapiens
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        SEQ ID NO 3933
LENGTH: 32220
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ORGANISM:
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                                                       1135 TATATATAGTATTTGTGGTAGAGATGGGATTTTTGCCATGTTGCCCAGGCTAGTATTGAAC
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     1; Gaps
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                                                                                                                                                                                                                                                                                                                                  131020 GCCACCGCAGCCGAAACTTTGTTTTTTTCCTCTTTTTGTTG 131065
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Publication No. US20030114399A1

GENERAL INFORMATION:
APPLICANT: BLAKELY, RANDY D.
APPLICANT: APPRESUNDARAM, SUBRAMANIAM
APPLICANT: FERGUSON, SHAWN
TITLE OF INVENTION: HUMAN AND MOUSE CHOLINE TRANSPORTER CDNA
FILE REFERENCE: VBLT.:008US
CURRENT APPLICATION NUMBER: US/09/911,077A
CURRENT FILING DATE: 2001-07-23
NUMBER OF SEQ DO NOS: 27

SOFTWARE: Patentin Ver. 2.1
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Sequence 3933, Application US/09764877

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFRENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877

CURRENT FILING DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 4031

SOFTWARE: Patentin Ver. 2.0
  37; Indels
  0; Mismatches
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LOCATION: (2347)..(90873)
COTHEN INFORMATION: N = A, C, G or T/U
US-09-911-077A-19
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LENGTH: 119040
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Matches 128;
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                                                                                                                                                                                                                                                                                     APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR PLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-04-20
PRIOR PLICATION NUMBER: US 60/193,483
PRIOR PLICATION NUMBER: US 60/193,483
PRIOR PLICATION NUMBER: US 60/195,218
PRIOR PLICATION NUMBER: US 60/185,218
PRIOR PLICATION NUMBER: US 60/185,218
PRIOR PLICATION NUMBER: US 60/167,363
PRIOR PLICATION NUMBER: US 60/156,358
PRIOR PLICATION NUMBER: US 60/156,358
PRIOR PLICATION NUMBER: US 60/146,002
PRIOR PLING DATE: 1999-10-29
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-80
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Sequence 95562, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR PELICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-04-20
PRIOR PELICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-02-24
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4.5%; Score 92.6; DB 12; Length 555;
Best Local Similarity 73.0%; Pred. No. 2.6e-13;
Matches 119; Conservative 0; Mismatches 44; Indels 0
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US-10-027-632-95562
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US-10-027-632-95563
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US-10-027-632-95563
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## PRIOR FILING DATE: 1999-11-23
| PRIOR PILLING DATE: 1999-09-28
| PRIOR PAPLICATION NUMBER: US 60/166,002
| PRIOR PAPLICATION NUMBER: US 60/146,002
| PRIOR PILLING DATE: 1999-09-28
| PRIOR FILING DATE: 1999-09-08-09
| PRIOR FILING DATE: 1999-09-08-09
| WUMBER OF SEQ 1D NOS: 325720
| SOFTWARE: FastSEQ for Windows Version 4.0
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Perfect score:

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Scoring table:

Word size

Database

Searched:

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Human cell witheri
Candida essential
Human map-related
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Human snp oligonuc
Mouse TNF-a hammer
Mouse TNF-a hammer
Human TNF-alpha ha
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Integrin subunit b
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ABN87490
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ABV74647
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AAT56350
AAT56332
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23-MAR-2001; 2001WO-CN00398
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                                                                                                                                                                                                            Human; mitotic cycle re
immunological disease;
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WO200175033-A2.
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probe; ss.
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10457.963 Million cell updates/sec
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an or equal to the score of the result being printed,
y analysis of the total score distribution.
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| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                 2552756 segs, 1349719017 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                             OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                               summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAI71558
AAI71555
AAI71557
ABA97055
AAQ57179
AAZ56029
AAH26599
                                                                                                                                                                                                        OLIGO_NUC
Gapop_60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       greater than or equal to derived by analysis of
                                                                                                                                            US-10-005-337A-2
2074
1 ctgcagcaagttactt
                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Listing first 45
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Query
Match Length D
                                                                                          November 14,
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Maximum DB seq length: 50
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Human, mitotic cycle regulation protein 9, cancer, haemopathy; immunological disease; HIV infection; inflammation; gene therapy;
                                                                                                                                                                    Human mitotic cycle regulation protein 9 cDNA probe #1.
                                                                                                                                                                                                                                                                                                                                                                                            (SHAN-) SHANGHAI BIO WINDOW GENE DEV INC.
  23-MAR-2001; 2001WO-CN00398
                                                                                                                                                                                                                                                                                                                                                                24-MAR-2000; 2000CN-0115092
                                                                                                                                           (first entry)
                                                                                      AAI71557 standard; DNA;
                                                                                                                                                                                                                                                                               WO200175033-A2
                                                                                                                                                                                                                                                                                                                                                                                                                       Mao Y, Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-MAR-2002
                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                           10-JAN-2002
                                                                                                                                                                                                                                                                                                           11-OCT-2001.
                                                                                                                 AAI71557;
                                                                                                                                                                                                                           probe; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABA97055;
                 30
                                                       ABA97055/
ID ABA9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
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                  엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                           ö
                                                                                 The present invention provides the protein and coding sequences of human mitotic cycle regulation protein 9. The sequences can be used in the treatment of cancer, heemopathy, HIV infection, immunological diseases and inflammation. The present sequence is a probe for the coding sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences of human mitotic cycle regulation protein 9. The sequences can be used in the treatment of cancer, haemopathy, HIV infection, immunological diseases and inflammation. The present sequence is a PCR primer for the coding
used in diagnosis and treatment of malignant tumors, hemopathy, human immunodeficiency virus infection, immunological diseases and inflammation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human mitotic cycle regulation protein 9 and encoded polynucleotide, used in diagnosis and treatment of malignant tumors, hemopathy, human immunodeficiency virus infection, immunological diseases and
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; mitotic cycle regulation protein 9; cancer; haemopathy; immunological disease; HIV infection; inflammation; gene therapy;
                                                                                                                                                                                                                           ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human mitotic cycle regulation protein 9 cDNA PCR primer #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22; Length 33;
13;
                                                                                                                                                                                              DB 22; Length 41; 4.4;
                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 33 BP; 12 A; 11 C; 3 G; 7 T; 0 other;
                                                                                                                                                                    Sequence 41 BP; 17 A; 12 C; 3 G; 9 T; 0 other;
                                                                                                                                                                                              Query Match
1.1%; Score 22; DB
Best Local Similarity 100.0%; Pred. No. 4.4
Matches 22; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.0%; Score 21; DB Best Local Similarity 100.0%; Pred. No. 13; Matches 21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BIO WINDOW GENE DEV INC.
                                                                                                                                                                                                                                                      1150 TGGTAGAGATGGGATTTTGCCA 1171
                                                                                                                                                                                                                                                                     22 TGGTAGAGATGGGATTTTGCCA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; Page 19; 33pp; Chinese.
                                                            Example 6; Page 21; 33pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2001; 2001WO-CN00398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAR-2000; 2000CN-0115092
                                                                                                                                                                                                                                                                                                                                                     AAI71555 standard; DNA; 33
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SHAN-) SHANGHAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200175033-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammation
                                                                                                                                                                                                                                                                                                                                                                                                          10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                               AAI 71555;
     used in
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                                                                                                                                                                                                                                                                                                                                    RESULT 2
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The present invention provides the protein and coding sequences of human mitotic cycle regulation protein 9. The sequences can be used in the treatment of canner, haemopathy, HIV infection, immunological diseases and inflammation. The present sequence is a probe for the coding sequence of the invention.
                                         Human mitotic cycle regulation protein 9 and encoded polynucleotide, used in diagnosis and treatment of malignant tumors, hemopathy, human immunodeficiency virus infection, immunological diseases and inflammation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, 2-hydroxy acid dehydrogenase 16; cancer; haemopathy; HIV;
human immunodeficiency virus; infection; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                    1.0%; Score 20; DB 22; Length 41;
100.0%; Pred. No. 41;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human 2-hydroxy acid dehydrogenase 16 PCR primer SEQ ID 6.
                                                                                                                                                                                                                                                                                                                                                                     Sequence 41 BP; 18 A; 11 C; 3 G; 9 T; 0 other;
                                                                                                                                                                        Example 6; Page 21; 33pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1152 GTAGAGATGGGATTTTGCCA 1171
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Best Local Similarity 100.
Matches 20, Conservative
WPI; 2001-626411/72.
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Indels

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1152 GTAGAGATGGGATTTTGCCAT 1172

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This is an AU-rich element (ARE) sequence used in competition studies to devaluate the role of ARE proteins in the process of RNA deadenylation or degradation. It is thought that AREs influence mRNA degradation rates. The invention relates to an in vitro system (consisting of a cell extract and an exogenous target RNA) that is able to recapitulate regulated RNA turnover of the target RNA. The system is used to dentify agents that modulate stability, deadenylation or degradation of the target RNA, or endogenous molecules that participate in deadenylation/degradation of the target RNA. These modulators e.g AREs are preferably involved in cell growth and differentiation in mammals, especially where these processes are implicated in cell transformation and immune system dysfunction and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AU rich element, ARE, adenylation, differentiation, rheumatoid arthritis, transcription template, inflammatory bowel disease, ss.
                                                                                                                                                                 This is a TNF-alpha mRNA target sequence (nucleotide no. 1344) of an enzymatic RNA molecule (ribozyme) which cleaves mRNA associated with the development or maintenance of a psoriatic or asthmatic condition. The concn. of the ribozyme necessary to effect a therapeutic treatment is lower than that of an antisense oligonucleotide and the specificity of action is higher.
                                      Enzymatic RNA molecules which cleave mRNA - used to treat or prevent inflammatory, arthritic, stenotic or cardiovascular diseases
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            In vitro system for studying regulated RNA turnover, containing cell
extract and target RNA, for identifying modulators of RNA stability,
                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                              Length 34;
                                                                                                                                                                                                                                                                                                                                                                          0.9%; Score 18; DB 15; Length 34
100.0%; Pred. No. 3.7e+02;
live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                     Seguence 34 BP; 10 A; 0 C; 0 G; 24 T; 0 other;
                                                                                                                                                                                                                                                                                            (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 53; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AU-rich element (ARE) sequence #1
                                                                                                                             Claim 3; Page 16; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              380 AAATAAATAAATAAA 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВР.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    extract and target RNA, for i potential therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US11581.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0086675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZS6029 standard; RNA; 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 100.(
Marches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYNE-) UNIV NEW JERSEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-086719/07.
      WPI; 1994-048853/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ford LP;
                                                                                    or conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ56029;
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                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel human 2-hydroxy acid dehydrogenase 16, its recombinant production, its encoding polymorlecticide and application and a 2-hydroxy acid dehydrocgenase 16 antagonist. The polypeptide is useful for treating cancer, haemopathy and human immunodeficiency virus infection. This sequence represents a PCR primer used in the amplification of the human 2-hydroxy acid dehydrogenase 16 described in the method of the invention.
                                                                                                                                                                                                                                                                                      New human 2-hydroxy acid dehydrogenase 16 and encoding polynucleotide, useful for treating cancer, haemopathy and human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumour necrosis factor; specific; cleavage; target RNA; protein; expression; inhibitor; inhibition; ribozyme; treatment; prophylaxis; prevention; psoriasis; asthma; inflammatory diseases; restenosis; cardiovascular condition; hypereension; arthritis; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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00.0%; Pred. No. 1.2e+02;
ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enzymatic RNA molecule TNF-alpha mRNA target sequence.
                                                                                                                                                                                                                                                                                                                                                                        Example 4; Page 19 (Disclosure); 33pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 33 BP; 8 A; 11 C; 4 G; 10 T; 0 other;
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                                                                                                                                                                 CO LTD SHANGHAI
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92US-0989848.
92US-0989849.
                                                                               24-MAR-2000; 2000CN-0115096
                                                                                                                        24-MAR-2000; 2000CN-0115096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                 (BODE-) BODE GENE DEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity
Thes 19; Conserva
                                                                                                                                                                                                                                                 WPI; 2002-056337/08.
                                                                                                                                                                                                        Mao Y, Xie Y;
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07-DEC-1992;
07-DEC-1992;
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                                        03-OCT-2001.
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CN1315516-A
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26-JUL-1994
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                                                                                                                                                                                                                                                                                                                                 infection
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19-SEP-2002
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                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                              Gene
                                                                                                                                                                                                                                                                                                                      ARE;
                                                                                                                                                                                                                                 RESULT 8
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are potential therapeutic agents, e.g. in conditions associated with abnormal expression of tumour necrosis factor-alpha. Examples of such diseases include sepsis, rheumatroid arthritis or inflammatory bowel disease. The system can also be used diagnostically to detect the molecular defects in such conditions and for development of improved gene
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Melanoma differentiation associated gene-7 promoter capable of treating cancer comprises directing transcription of heterologous coding sequence encoding tumour suppressor polypeptide positioned downstream, useful for treating cancer -
                                                                                     ö
                                                                    0.9%; Score 18; DB 21; Length 34;
100.0%; Pred. No. 3.7e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                    Human tumour necrosis factor gene 3' UTR AU-rich element.
                                                                                   Indels
                                                                                                                                                                                                                   Tumour necrosis factor; human; AU-rich element; ss.
                                                      Sequence 34 BP; 10 A; 0 C; 0 G; 24 U; 0 other;
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"AUUUA motif"
                                                                                                                                                                                                                                                                                              "AUUUA motif"
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                                                                                                   380 AAATAAATAAATAAA 397
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"AUUUA
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                                                                           Best Local Similarity 100.
Matches 18; Conservative
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                                       delivery systems
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                                                                                                                                                                                                                                                       misc_feature
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AAH26599/c
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                                                                                                             untranslated region (3'UTR) of human tumour necrosis factor mRNA.

The presence of AU-rich elements (ARBS) in eukaryotic mRNAs correlates with rapid mRNA turnover and post-translational control.

The ARB consists of multiple AUUVA motifs or sequences resembling it. A similar ARE sequence is found in the 3' UTR of the human melanoma differentiation associated gene-7 (Mda-7) gene (see AAH26596). The invention provides recombinant expression constructs in which the human Mda-7 promoter (see AAH26595) is operably linked to a coding sequence encoding a tumour suppressor protein. A pharmaceutical composition including the recombinant expression construct is used in a claimed method of treating melanoma, neuroblastoma, astrooftoma, glioblastoma multiforme, cervical cancer, colon cancer, prostate cancer, osteosarcoma, chondrosarcoma or a cancer of the central nervous system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression; transcript stability; drug screening; AU-rich element; tumour necrosis factor; TNF; ds.
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                                                                               sequence is that of an AU-rich sequence in the 3'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18; DB 22; Length 34;
Pred. No. 3.7e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumour necrosis factor (TNF) AU-rich element (ARE) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 34 BP; 10 A; 0 C; 0 G; 24 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Prec.
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Disclosure; Fig 2C; 132pp; English.
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Matches 18; Conservative
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                        targets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transcript stability; drug screening; AU-rich element;
of a polynucleotide of interest. They are useful for modulating gene expression, identifying and analysing regulatory sequences, new targets and reagents for treating human diseases and for drug screening. The present sequence is tumour necrosis factor (TNF) ARE (AU-rich element) DNA. This sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New expression vector useful for modulating gene expression, identifying and analyzing regulatory sequences, new targets and reagents for treating human diseases, comprises a transcribable
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                                                                                                                                              Length 34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour necrosis factor (TNF) AU-rich element (ARE) RNA.
                                                                                                                                          0.9%; Score 18; DB 24; I
100.0%; Pred. No. 3.7e+02;
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                                                                                                            Sequence 34 BP; 10 A; 0 C; 0 G; 24 T; 0 other;
                                                                                                                                                                                   Mismatches
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                                                                                                                                          0.9%,
100.0%; Pre-
                                                                                                                                                                                                                     380 AAATAAATAAATAAA 397
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                                                                                                                                                                                                                                                                                                                                              AAD46934 standard; RNA; 34 BP
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                                                                                                                                                              Best Local Similarity
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                                                                                                                                                                                 18;
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The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl Nydrocarbon nuclear transporter (ARNY) gene, an integrin subunit beta 3 gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16675 to AAA17165 to AAA1762 represent ribozyme sequences for AAA1769 to AAA1769 and AAA1168 to present their corresponding target sequences; AAA11685 to AAA19185 to AAA2189 and AAA2189 to AAA2180 to AA
                                                                                                                                                                                                                                                                                                                                                   Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic; ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; verruca vulgaris; angiofibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; ss. Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an angiogenic factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coeshott C, McSwiggen JA;
                                                                                                                                                                                                                                                                                                         Integrin subunit beta 3 substrate sequence SEQ ID NO:5922.
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BP.
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                                                                                                                                                        AAA22696 standard; RNA; 17
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Length 34;

0.9%; Score 18; DB 24; I 00.0%; Pred. No. 3.7e+02;

Sequence 17 BP; 4 A; 0 C; 0 G; 13 U; 0 other;

Query Match Best Local Similarity 100.( Matches 18; Conservative

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The present invention describes enzymatic nucleic acid molecules with Max Cheaving activity, which specifically cleave RNA encoded by an aryl hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3 gene, an integrin subunit beta 3 gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a Tia-2 gene. AAA1767 to AAA1768 to AAA2169 to AAA2168 to AAA2169 to AAA2169 to AAA2168 to AAA2169 to AAA2168 to AAA218 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic; ophthalmologic; antidiamatory; antiarthritic; antipsoriatic; ARMD; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; veruca vulgaris; angiofibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
                                                                                                                            Gaps
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                                Length 17;
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                                DB 20; L
1.1e+03;
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                                Score 17;
Pred. No.
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0.8%; Scc.
100.0%; Pred
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                                                                                                                                                                                                               381 AATAAATAAATAAA 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA22697 standard; RNA; 17 BP.
                                                                                                                                                                                                                                                                                                  17 AATAAATAAATAATAA 1
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                  Query Match 0.8 Best Local Similarity 100. Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
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This is a transcription template sequence for an AU rich element (ARE)

protein. The synthetic oligonucleotide is used in evaluation of the role

of ARE proteins in the process of RNA deadenylation or degradation. It is

thought that AREs influence mRNA deadenylation or degradation. It is

thought that AREs influence mRNA deadenylation or degradation. It is

to an in virro system (consisting of a cell extract and an exogenous

crarget RNA) that is able to recapitulate regulated RNA turnover of the

target RNA. The system is used to identify agents that modulate

stability, deadenylation or degradation of the target RNA. These modulators e.g AREs are preferably involved in cell growth and

fiferentiation in mammals, especially where these processes are

implicated in cell transformation and immune system dysfunction and are

potential therapeutic agents, e.g. in conditions associated with abnormal

expression of tumour necrosis factor-alpha. Examples of such diseases. The

include sepsis, rheumandation arthritis or inflammatory bowel disease. The

system can also be used diagnostically to detect the molecular defects in

cut conditions and for development of improved gene delivery systems.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    rheumatoid arthritis;
and other syndromes and diseases related to the levels of ARNT, Tie-2, integrin subunit alpha-6, or integrin subunit beta-3.
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                                                                                                                                   Gaps
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                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AU rich element; ARE; adenylation; differentiation;
transcription template; inflammatory bowel disease;
                                                                                             Score 17; DB 20; I
Pred. No. 1.1e+03;
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                                                          Sequence 17 BP; 4 A; 0 C; 0 G; 13 U; 0 other;
                                                                                                      100.0%; Pred. ...
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Best Local Similarity
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Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis; integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic; ophthalmologic; antinflammatory; antiarthritic; antipsoriatic; ARMD; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; vertuca vulgaris; angiofibroma; tuberous sclerosis; pot-wine stain; Sturge Weber syndrome; ss.
                         Integrin subunit beta 3 substrate sequence SEQ ID NO:5924.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel ribozymes for modulating the synthesis, expres
stability of an mRNA encoding an angiogenic factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 54; Page 236; 305pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PA, Roberts E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-591315/50.
                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                              WO9950403-A2
                                                                                                                                                                                                                                                                                                                                                                       24-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to DNA topoisomerase II 12.76 (ABB99905) and nucleic acids encoding it (ABQ77974). The protein has a molecular weight of 13 kD. The invention also relates to a method for the recombinant production of the protein, an antagonist of the protein, and the use of the protein, gene and antagonist in therapeutic applications. DNA topoisomerase II 12.76 can be used in the treatment of a variety of diseases such as malignant tumours, blood diseases, HIV (human immunodeficiency virus) infection, immune disorders and inflammatory conditions. Sequences ABQ77984 sepresent PCR primers used in an exemplification of the invention to amplify DNA topoisomerase II 12.76
                                                                                                                                                                                                                                                                                    DNA topoisomerase II 12.76; recombinant production; gene therapy; malignant tumour; cancer; blood disease; HIV infection; human immunodeficiency virus; immune disorder; inflammatory condition; cytostatic; antiinflammatory; immunomodulator; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polypeptide-DNA topoisomerase II 12.76 and polynucleotide for encoding the polypeptide, useful for curing several diseases, such as malignant tumor, hemopathy, HIV infection, immunological disease and
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100.0%; Pred. No. 1.1e+03
ive 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1242 TIACAGGIGIAAGCCAC 1258
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                     21 AATAAATAAATAAA
                                                                                                                                 ABQ77985 standard; DNA; 33
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                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
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expression and/or

McSwiggen JA;

Coeshott C,

Jarvis T,

98US-0079678.

99WO-US06507.

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The present invention describes enzymatic nucleic acid molecules with CRNA cleaving activity, which specifically cleave RNA encoded by an aryl hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA17675 and AAA17661 to AAA17623 to AAA17684 represent their corresponding target sequences AAA17685 to AAA181836 and AAA19087 to Corresponding target sequences; AAA19154 represent riboxyme sequences for Tie-2, and AAA18186 to AAA19086 and AAA19155 to AAA19223 to AAA20361 to AAA21595 represent their corresponding target sequences; CC AAA19155 to AAA21680 represent triboxyme sequences for integrin alpha 6 subunit, and AAA21502 to AAA21500 and AAA21596 to AAA21680 represent their corresponding target sequences; CC AAA21595 to AAA21501 to AAA21591 represent riboxyme sequences for integrin subunit beta 3, and AAA23476 to AAA21342 represent their corresponding target sequences; CAAA21592 to AAA2159 to AAA22334 to AAA2159 to AAA2159 to AAA2159 to AAA2159 to AAA2159 to The invention are used for modulating the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially ase related contegrin subunit beta 3, integrin subunit alpha-6, or Tie-2. They are especially used to treat cancer, dabetic retinopathy, age related concerned angular degeneration (ARND), inflammation, and archritis, as well as conceved and others syndrome, of tuberous sclerosis, pot-wine stains, Sturge Weber conductor and diseases related to the levels of ARNT, Tie-2, and other syndromes and diseases related to the levels of ARNT, Tie-2, and others syndromes and others concerned to the levels of ARNT, Tie-2, and others syndromes and others concerned to the levels of ARNT, Tie-2, and others syndromes and others and others.
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AAA22698 standard; RNA; 17

RESULT 14 AAA22698/

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19-JUN-2000 (first entry)

AAA22698;

RESULT 15 AAA22708/c

integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme; hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic; ophthalmologic; antiinflammatory; antiatrhritic; antipsoriatic; ARMD; dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis; age related macular degeneration; inflammation; neovascular glaucoma; myopic degeneration; psoriasis; veruca vulgaris; angiofibroma; tuberous sclerosis; pot-wine stain; studer syndrome; Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss. aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis; Novel ribozymes for modulating the synthesis, expression and/or stability of an mRNA encoding an anglogenic factors Coeshott C, McSwiggen JA; Integrin subunit beta 3 substrate sequence SEQ ID NO:5934. Claim 54; Page 237; 305pp; English Jarvis T, AAA22708 standard; RNA; 17 BP 98US-0079678. 99WO-US06507 (RIBO-) RIBOZYME PHARM INC 19-JUN-2000 (first entry) Pavco PA, Roberts E, WPI; 1999-591315/50. Homo sapiens. WO9950403-A2. 24-MAR-1999; 27-MAR-1998; 07-OCT-1999 AAA22708; 

The present invention describes enzymatic nucleic acid molecules with RNA cleaving activity, which specifically cleave RNA encoded by an aryl Nydrocarbon nuclear transporter (ARNY) gene, an integrin subunit beta 3 gene, an integrin subunit beta 3 gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to AAA17651 to AAA17651 to AAA17655 and AAA17684 represent their corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to AAA19155 to AAA419522 represent their corresponding target sequences; and AAA41055 to AAA41955 to AAA41688 represent their corresponding target sequences; AAA21689 to AAA421631 and AAA21635 to AAA21635 to AAA21639 to AAA421635 and AAA21635 to AAA21639 to AAA421635 and AAA21635 to AAA21639 to AAA21635 and AAA21635 to AAA21639 to AAA421635 to AAA21639 to AAA421635 to AAA23163 to AAA23162 to AAA23163 to AAA23163 to AAA23163 to AAA23162 to AAA23162 to AAA23163 to AAA23162 to AAA23163 to AAA23162 to AAA23162 to AAA23162 to AAA23163 to AAA23162 to AAA23163 to AAA23162 to AAA23163 to AAA2316 integrin subunit alpha-6, or integrin subunit beta-3

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Query Match 0.8%; Score 16; DB 20; Length 17; Best Local Similarity 100.0%; Pred. No. 3.4e+03; Matches 16; Conservative 0; Mismatches 0; Indels 378 AAAAATAAATAAATAA 393 ||||||||||||||||

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AZ33322 1M0062P08
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28 bp mRNA linear EST 11-OCT-1995
yr49804.sl Soares fetal liver spleen lNFLS Homo sapiens cDNA clone
IMAGE:208494 3' similar to gb|M87917|HUMALNE441 Human carcinoma
cell-derived Alu RNA transcript, (TRNA); gb:M91159 !!!! ALU CLASS EMARNING ENTRY !!!! (HUMAN);, mRNA sequence.
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1 (bases 1 to 28)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, P., Trevaskis, E., Waterston, The WashU-Merck EST Project
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AZ331633 1M0059N11
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fal: 314 286 1800
Fax: 1850 1810
Email: est@watson.wustl.edu
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TA194C08P
N27542
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Contact: Wilson RK
  Homo sapiens
  RESULT 1
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AUTHORS
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Dictyostelium discoideum
Eukaryostelium discoideum
Eukaryostelium, discoideum
1 (bases 1 to 38)
Urushihara, H., Morio, T., Saito, T., Koriki, E., Ochiai, H., Maeda, M., Takeuchi, I., Kohara, Y. and Tanaka, Y.
Population analysis of CoNAs from unicellular and multicellular stages of Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                        double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
                  for further information.
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Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
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                IMAGE Consortium (info@image.llnl.gov) Frace considered overall poor quality
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Std Error: 0.00
                                                                                                                                                  /organism="Homo sapiens"
/mol type="mRNN"
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/db_xref="texon:9606"
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Location/Qualifiers
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Seq primer: Promega -21ml3
High quality sequence stop: 1.
Location/Qualifiers
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/strain="AX4"
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1 (bases 1 to 32)

1 Hillar, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkhi, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, T.R., Williamson, A., Wohldmann, P. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 bp mRNA linear EST 26-OCT-1995
yu18h07.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:234205 3′ similar to gb:D10202 PLATELET ACTIVATING FACTOR
Insert Size: 3194
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Trace considered std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
Insert Size: 1926
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 28;
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1.2e+04;
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100.0%; Pred. No. ...
                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3777625"
/db_xref="taxon:9606"
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                                                                                                                                                  Insert Length: 3194 Std Error
Seg primer: Promega -21m13
High quality sequence stop: 1.
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Homo sapiens
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Best Local Similarity 100.
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Submitted (21-007-2002) Weisshaar B., Max-Planck-Institut fuer Submitted (21-007-2002) Weisshaar B., Max-Planck-Institut fuer Suechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone MCK7. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:
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Arabidopsis thaliana T-DNA flanking sequence GK-276A12-015154,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sparmatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B., A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H. and Weisshaar, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines
                                                                                                                                                                                                                                                                                              /organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
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Li,Y., Rosso,M., Strizhov,N. and Weisshaar,B.
Direct Submission
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100.0%; Pred. No. 1.2e+04;
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                                                                                                                                                                                                                                               Email: hideko@biol.tsukuba.ac.jp
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                       /sex="mat A"
/dev_stage="vegetative"
/clone_lib="VS"
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/clone="VSH886"
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                                                                                                                                                                                                              EST 02-MAR-2001
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: frazer.murray@bbsrc.ac.uk
GCGGCCCGCTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetech
                                                       Gaps
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0.9%; Score 18; DB 9; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 18; Conservative 0; Mismatches 0; Indels
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                0.9%; Score 18; DB
100.0%; Pred. No. 1.2
ative 0; Mismatches
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/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:901"
/clone="ROS071D10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roslin Institute
Roslin, Midlothian, EH25 9P8,
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer, murray@bbsrc.ac.
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Dictyostelium discoideum
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Gallus gallus
                                                                                                           Unpublished
Contact: Frazer Murray
                   Query Match 0.99
Best Local Similarity 100.(
Matches 18; Conservative
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                                                                                                                                  About the Arabidopsis that the Arabidopsis that insertion lines" (Clone-"DCK was performed on DNA from Arabidopsis that plants (T1) which were transformed with the T-DNA from Proceed page (T1) which were transformed with the T-DNA from vector page (T1) which were transformed with the T-DNA from vector page (T1) which were transformed with the T-DNA from vector page (T1) which were transformed with the T-DNA from vector page (T1) which were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thalaina nuclear genome sequence were processed for submission. T-DNA derived sequences were
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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2M0098P11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0098P11 F, genomic survey sequence.
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
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                                                                   /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0098 row: P column: 11
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
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/clone="UUGC2M0098P11"
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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwh02 (gi|4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
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/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0258 row: G column: 09
Seg primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
                                                                     Laboratory Mouse DNA Resource
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/clone="UUGC2M0258G09"
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Mus musculus
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                                                                                        (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AFL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-completent E. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
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1M0062P08F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0062P08 F, genomic survey sequence.
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University of Utah Genome Center
University of Utah
Nuiversity of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 184112, USA
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Unpublished
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100.0%; Pred. No. 8.8e+04;
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Insert Length: 10000 Std Error: 0.00
                                                                              Laboratory Mouse DNA Resource
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Best Local Similarity 100.0%; Préd. No. 8.86
Matches 16; Conservative 0; Mismatches
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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Location/Qualifiers
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Fax: 801 585 7177
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AZ333223/c
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (4)14732144[4p]APL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Menen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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1M0031B16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0031B16 F, genomic survey sequence.
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42Iv; Purified genomic DNA from M.
musculus C57BL/6J (Male) was obtained from the Jackson
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Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
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                                                                                                                                  Laboratory Mouse DNA Resource
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/clone="UUGC1M0031B16"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Mus musculus
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Plate: 0031 row: B
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clone="UUGC1M0080P08"
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ345473
1M0080P08F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0080P08 F, genomic survey sequence.
                    /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M.musculus G57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: P column: 08
Seg primer: CGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 25.
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/strain="C578L/6J"
/db_xref="taxon:10090"
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Mus musculus
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil 4732114 [gb] AFL25072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-complement S. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Insert Size: 964
High qality sequence stops: 1
Source: IMAGE Consortium, LLNL This clone is available royalty-free
through LLNL, contact the IMAGE Consortium (info@image.llnl.gov)
for further information. Trace considered overall poor quality
Insert Length: 964 Std Error: 0.00
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1 (bases 1 to 27)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldman,P. and Wilson,R.
                                                                                                           from the Jackson
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from
musculus C57BL/6J (male) was obtained from the Jackson
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 2.3e+05;
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U. (*);

Best Local Similarity 100.0%; Pred. No. 2.36
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High quality sequence stop: 1
Location/Qualifiers
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Email: est@watson.wustl.edu
Insert Size: 3006
High qality sequence starts: 1 High qality sequence stops: 1
Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL, contact the IMAGE Consortium (inf@@image.llnl.gov)
for further information. Trace considered overall poor quality Insert Length: 3006 Std Error: 0.00
Seq primer: -21ml3
High quality sequence stop: 1.
Location/Qualifiers
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1 (bases 1 to 28)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                         165402 28 dp mRNA linear EST 07-MAR-1995 yc73d01.51 Soares infant brain lNIB Homo sapiens cDNA clone IMAGE:21732 3' similar to 9B] M879171 HUMALNE41 Human carcinoma cell-derived Alu RNA transcript, (rRNA); gb:304513 HEPARIN-BINDING GROWTH FACTOR PRECURSOR 2 (HUMAN); mRNA sequence.
                                                            Gaps
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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     Length 28;
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  0.7%; Score 15; DB 9; L. 100.0%; Pred. No. 2.3e+05; ve 0; Mismatches 0;
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/db_xref="GDB:394079"
/db_xref="taxon:9606"
/clone="IMAGE:21732"
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     100.0%; Pre-
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Homo sapiens
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Query Match 0.7
Best Local Similarity 100.
Matches 15; Conservative
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Fax: 314 286 1810
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Best Local Similarity
Matches 15; Conservat
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/mol_type="mRNA"
/db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https://db_txef="https
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ok57f12.s1 NCI CGAP Lei2 Homo Sapiens CDNA clone IMAGE:1518095 3' similar to TR:Q41805 Q41805 EXTENSIN-LIKE PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 28)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               constructed by Bento Soares and M. Fatima Bonaldo."
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0
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100.0%; Pred. No. 2.3e+05;
live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
unknown library type
Trace considered overall poor quality
Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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/db_xref="GDB:479080"
/db_xref="taxon:9606"
/clone="IMAGE:126919"
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                                                                                  /sex="male"
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Homo sapiens
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Unpublished
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University of Utah Genome Center
University of Utah
Francis Of Utah
Francis Of Utah
Francis Of Utah
Francis Of Office Office
                                                                                                                                                                                                                                                                                                   AZ345640 100080124F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0080124 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. L (basea 1 to 28)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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Fax: 801 585 7177
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: I column: 24
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plaamid ends
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/strain="C57BL/6J"
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Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ345640.1 GI:10424877
      10 TGGGATTACAGGTGT 24
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28 AAAATAAATAAATAA 14
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Search completed: November 14, 2003, 19:05:52 Job time : 4320.19 secs

379 AAAATAAATAA 393

Query Match
0.7%; Score 15; DB 28; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 15; Conservative 0; Mismatches 0; Indels

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ZIP. 90017

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM COMPATIBLE
OPREATING SYSTEM: IBM MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,503
FILING DATE: 04-MAY-1995
CLASSIFICATION NUMBER: US/08/434,503
FILING DATE: 19-JAN-1995
APPLICATION NUMBER: US/089,849
FILING DATE: 19-JAN-1993
APPLICATION NUMBER: US/089,849
FILING DATE: December 7, 1992
APTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
                                                                                                 US-09-422-978-10125
US-08-859-998-147
US-09-225-928-147
US-09-225-228-147
US-09-641-638-1027
US-09-641-638-1027
US-09-422-978-488
US-09-422-978-488
US-09-422-978-3399
US-08-171-389-18
US-08-171-389-18
US-08-171-389-18
US-08-475-23A-18
US-08-475-23A-18
US-08-354-947-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 29, Application US/08434503
Patent No. 5616490
GENERAL INFORMATION:
APPLICANT: Sean M. Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: METHOD AND REACENT FOR
TITLE OF INVENTION: DISEASE
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
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60;
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                         PCT-US95-10202-3
PCT-US95-10203-3
PCT-US95-10220-3
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Best Local Similarity 100.0%; Pred. No.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 34
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
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Sequence 3
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Sequence 5
Sequence 5
Sequence 7
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-176-682-18
US-09-422-978-4951
US-09-422-978-2343
US-09-422-978-2343
US-09-422-978-2343
US-08-311-486C-1991
US-08-311-486C-1991
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US-08-311-486C-713
US-08-311-486C-714
US-08-311-486C-715
US-08-483-553-3
US-08-483-553-3
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US-09-791-211-75
US-09-918-686-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              569978 segs, 220691566 residues
                                                                                                                                sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                        OLIGO_NUC
Gapop_60.0 , Gapext 60.0
                                                                                                                              - nucleic search, using
                                                                                                                                                                                                                                                                                              US-10-005-337A-2
2074
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Match
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                                                                                                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
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Database :

Result No.

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Word size

Searched:

Sequence:

Matches

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GENERAL INFORMATION:

APPLICANT: Cohen, Daniel

APPLICANT: Cohen, Daniel

APPLICANT: Blumenfeld, Marta

APPLICANT: Blumenfeld, Marta

APPLICANT: Blumenfeld, Marta

FILE REPERENCE: GENSET.020CP1

FILE REPERENCE: GENSET.020CP1

CURRENT APPLICATION NUMBER: US 09/298,850

EARLIER APPLICATION NUMBER: US 09/298,850

EARLIER PILING DATE: 1999-10-20

EARLIER PILING DATE: 1998-11-23

EARLIER APPLICATION NUMBER: US 60/109,732

EARLIER PILING DATE: 1998-11-23

EARLIER FILING DATE: 1998-11-23

EARLIER FILING DATE: 1998-04-21

NUMBER OF SEQ ID NOS: 11796

SEQ ID NO 4951

LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Blougueleret, Lydie
APPLICANT: Chumakov, Ilya
APPLICANTON BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
FILE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REPRENCE: GENSET: 0510P1
CURRENT APPLICATION NUMBER: US 09/502,330
FRIOR PLILING DATE: 2000-02-11
FRIOR APPLICATION NUMBER: US 00/133,200
FRIOR PLILING DATE: 1999-03-23
FRIOR APPLICATION NUMBER: US 09/275,267
FRIOR APPLICATION NUMBER: US 06/119,917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: upstream amplification primer 99-18974 for SEQ 1017, US-09-422-978-4951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: allele
LOCATION: 21
LOCATION: 21
COTHER OF TITIT
US-09-641-638-1292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.8%; Score 16; DB 4; Length 19; Best Local Similarity 100.0%; Pred. No. 5.5e+02; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
US-09-641-638-1292/c
; Sequence 1292, Application US/09641638
; Patent No. 6432648
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Bougueleret, Lydie
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ORGANISM: Homo Sapiens
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: primer_bind
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APPLICANT: POWEr, Christopher
APPLICANT: POWEr, Michael B.
TITLE OF INVENTION: ANTISENSE OLIGODEOXYNUCLEOTIDES REGULATING EXPRESSION
TITLE OF INVENTION: ANTISENSE OLIGODEOXYNUCLEOTIDES REGULATING EXPRESSION
TITLE OF INVENTION: OF TNF-ALPHA
FILE REFERENCE: 3345.00002 US/09/176,862B
CURRENT APPLICATION NUMBER: 60/062,718
EARLIER PELLING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 18
LENGTH: 30
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; Sequence 44, Application US/09280409
; Patent No. 6107092
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Bert W. O'Malley
; TITLE OP INVENTION: ANTISENSE MODULATION OF SRA EXPRESSION
; FILE REFERENCE: RTS-0048
; CURRENT APPLICATION NUMBER: US/09/280,409
; CURRENT FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 146
; SEQ ID NO 44
; LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.8%; Score 17; DB 3; Length 30;
100.0%; Pred. No. 1.8e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 18;
Indels
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0.8%; Score 16; DB 3; Le.
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 0;
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US-09-280-409-44
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
US-09-422-978-4951
; Sequence 4951, Application US/09422978
                                                                                                                                                                                                                   RESULT 2
US-09-176-862-18
Sequence 18, Application US/09176862B
; Patent No. 6046319
                                                             380 AAATAAATAAATAAA 397
                                                                                                                        33 AAATAAATAAATAAA 16
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.8%
Best Local Similarity 100.0
Matches 17; Conservative
18; Conservative
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                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CALF: 940/1-2006
CALF: 940/1-2006
CAMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: 1BM Compatible
OPERATING SYSTEM: 1BM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,486C
FILING DATE: September 23, 1994
CLASSIFICATION DATA: including application
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: including application
APPLICATION NUMBER: 08/008/895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
                  Pred. No. 5.5e+02;
                                                                                                                                                                                                                                 Sequence 191, Application US/08311486C
Patent No. 5811300
GENERAL INFORMATION:
APPLICANT: Seas Sullivan
APPLICANT: Kevin Kisich
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: TNF-'
NUMBER OF SEQUENCES: 1157
CORRESPONDENCE
APPLICANT: ADDRESS:
                                        Mismatches
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 191: SEQUENCE CHARACTERISTICS: LENGTH: 15 hase a room
                                                                                   1253 AGCCACTGCACCGGC 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION: (213) 489-41600
TELEFRAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382 ATAAATAAATAA 396
                                                                                                                             21 AGCCACTGCACCCGGC
              Best Local Similarity 100.
Matches 16; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 15; Conserv
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US-08-311-486C-191/c
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                                                                                                                                    US-09-422-978-2343

i Sequence 2343, Application US/09422978
i Patent No. 6537751
i GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Chumakov, 11ya
i APPLICANT: Chumakov, 11ya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENERY 2000-1
CURRENT APPLICATION NUMBER: US/09/422, 978
CURRENT FILING DATE: 1999-04-21
EARLIER PILING DATE: 1999-04-21
EARLIER FILING DATE: 1999-04-21
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 2343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, 11ya
TITLE OF INVENTION: Bialelic markers for use in constructing a high density...
FILE REPERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT PILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-10-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: allele
COATION: 24
COATION: 99-10521-296 : polymorphic base C or T
US-09-422-978-2343
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LOCATION: 24
OTHER INFORMATION: 99-11685-200 : polymorphic base T or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.8%; Score 16;
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Patent No. 6537751
GENERAL INFORMATION:
           378 AAAAATAAATAA 393
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                                                      25 AAAAATAAATAA 10
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SEQ ID NO 2541
LENGTH: 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-422-978-2541/c
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Length 15;
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STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
ZOMPUTER READABLE FORM:
MEDIUM TYPE: 31. Diskette, 1.44 Mb
MEDIUM TYPE: 18. Ecorage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 03/08/311,486C
FILING DATE: September 23, 1994
CLASSIFICATION DATA: including application
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 03/09/849
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRAATION NUMBER: 2016/166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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US-08-311-486C-200/C
Sequence 200, Application US/08311486C
GENERAL INFORMATION:
APPLICANT: Sean Sullivan
APPLICANT: Remeth Draaper
APPLICANT: Remeth Draaper
APPLICANT: Dan T. Stinchcomb
APPLICANT: Janes McSwiggen
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: TAP-'
TITLE OF INVENTION: TAP-'
NUMBER OF SEQUENCES: 1157
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.7%; Score 15; DB 1;
                        TITLE OF INVENTION: RIBÓZYME TREATMENT OF
TITLE OF INVENTION: DISBASES OR CONDITIONO
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: TNP-'
NUMBER OF SEQUENCES: 1157
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
ADPRESSEE: Lyon & Lyon
                                                                                                                                                                                               ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.7%; Sc
Best Local Similarity 100.0%; P:
Matches 15; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 199
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          382 ATAAATAAATAA 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 15 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              us-08-311-486C-199
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                                                                        APPLICANT: Sean Sullian
APPLICANT: Dan T. Stinchcomb
APPLICANT: Day BARES: 1157
CORRESSEB: Lyon & Lyon
STREET: Sulte 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-206
COMPUTER: BADABLE PORM:
MEDIUM TYPE: Storage
COMPUTER: Sulte 4700
CITY: Los Angeles
STATE: Jan Word Perfect 5.1
COMPUTER: Sulte 4700
CITY: Los Angeles
STATE: Jan Word Perfect 5.1
COMPUTER: Sulte 4700
CITY: Los Angeles
STATE: Jan Word Perfect 5.1
COMPUTER: Sulte 4700
CITY: Los Angeles
STATE: Jan Word Perfect 5.1
COMPUTER: Sulte 4700
CITY: Los Angeles
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COMPUTER: Sulte 4700
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CITY: Los Angeles
STATE: Jan Word Perfect 5.1
COMPUTER: Sulte 4700
COMPUTER: Sulte 4700
COMPUTER: Sulte 4700
CITY: Los Angeles
STATE: Jan Word Perfect 5.1
COMPUTER: Sulte 4700
COMPUTER:
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US-08-311-486C-192/c
; Sequence 192, Application US/08311486C
; Patent No. 5811300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 381 AATAAATAAATA 395
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Best Local Similarity 100.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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Sequence 199, Application US/08311486C
Patent No. 5811300
GENERAL INFORMATION:
APPLICANT: Sean Sullivan
APPLICANT: Kenneth Draper
APPLICANT: Kevin Kisich

US-08-311-486C-199/c

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                                                                                                                                                                             CHERALING STRIEM: 18M F.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 0.80/311,486C
FILLING DATE: September 23, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application PRIOR APPLICATION DATA: described below:
PRIOR APPLICATION DATA: described below:
PRIOR APPLICATION DATA: described below:
PRIOR APPLICATION NUMBER: 07/989,895
FILLING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILLING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,327
REFERENCE/POCKET NUMBER: 209/166
TELEPHONE: (213) 955-0440
TELEFRAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sean Sullivan
APPLICANT: Sean Sullivan
APPLICANT: Kenneth Draper
APPLICANT: Kenneth Draper
APPLICANT: Kenneth Draper
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
TITLE OF INVENTION: TREATMENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.7%; Score 15; UD Best Local Similarity 100.0%; Pred. No. 1.7 Matches 15; Conservative 0; Mismatches
                  MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READBABLE FORM:
MEDIUM TYPE: S.5" Diskette, 1.44 Mb
                                                                 MEDIUM TYPE: storage
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/311,486C
FILING DATE: September 23, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 712, Application US/08311486C Patent No. 5811300
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            380 AAATAAATAAAT 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-311-486C-712/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: ]
US-08-311-486C-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                            STREET: 633 West Fifth Street
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-206
COMPUTER: EADABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: BACARGE
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,486C
FILING DATE: September 23, 1994
CLASSIFICATION DATA:
RICHARD APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: WASTENCE FOR STATES ATTORNEY AND STATES ATTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.7%; Score 15; DB 1; L. 100.0%; Pred. No. 1.7e+03; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RELATED TO LEVELS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/166
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: (7-3510
INPORTATION FOR SEQ ID NO: 200: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Pre-
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633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              381 AATAAATAAATA 395
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TITLE OF INVENTION: DISEASES
TITLE OF INVENTION: THE-ATED
TITLE OF INVENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 AATAAATAAATA 1
         Lyon & Lyon
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Best Local Similarity 100.
Matches 15; Conservative
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SS: single
linear
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SILVE SUITE COURTY: LOS ANGELES COURTY: LOS ANGELES CALIFORNIA
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: US-08-311-486C-200
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
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Length 15;
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 5.0 COMPUTER: 1BM COMPATIBLE
OPERATING SYSTEM: 1BM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA: 435
PILING DATE: September 23, 1994
CLASSIFICATION DATA: including application PRIOR APPLICATION DATA: including application PRIOR APPLICATION DATA: described below: APPLICATION DATA: 19, 1993
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/899,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INCRMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   0.7%; Score 15; DB 1; L. 100.0%; Pred. No. 1.7e+03; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Sean Sullivan
APPLICANT: Kevin Kisich
APPLICANT: Kevin Kisich
APPLICANT: Dan T. Stinchcomb
APPLICANT: Dan T. Stinchcomb
APPLICANT: Dan S REWAIgen
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: TNF-'
NUMBER OF SEQUENCES: 1157
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-08-311-486C-714/c
; Sequence 714, Application US/08311486C
; Patent No. 5811300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                           NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/1
TELEPOMUNICATION INFORMATION:
TELEPOMOR: (213) 955-0440
TELEK: (213) 955-0440
TELEK: (273510
INFORMATION FOR SEQ ID NO: 713:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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LECOMMUNICATION ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FELECOMMUNICATION INFORMATION:
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: (213) 955-0440
67-3510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,3
                           ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                 linear
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US-08-311-486C-713
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY AGENT INFORMATION:
NAME: Warburg, Richard J.
REFERENCE FOCKET NUMBER: 209/166
TELEPAN: (213) 955-0440
TELEPAN: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 712:
SEGUINGE CHARACTERISTICS:
LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
FILING DATE: December 7, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-08-311-486C-713/C

i Sequence 713, Application US/08311486C

i Patent No. 5811300

i GENERAL INFORMATION:
APPLICANT: Sean Sullivan
APPLICANT: Kenneth Draper
APPLICANT: Kenneth Draper
APPLICANT: Dan T. Stinchcomb
APPLICANT: Dan T. Stinchcomb
APPLICANT: Dan Sean Sullivan
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: TNF-'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,486C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     382 ATAAATAAATAA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 ATAAATAAATAA 1
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-311-486C-712
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OLISH WINTE TOWN SHILL

Sequence 18, Appl Sequence 669, Appl Sequence 627, Appl Sequence 650, Appl Sequence 933, Appl Sequence 135, Appl Sequence 136, Appl Sequence 720, Appl Sequence 720, Appl Sequence 720, Appl Sequence 361, Appl

Sequence 65, P Sequence 66, P Sequence 67, P

785, App 13, App 317, App 673, App 1831, App 1868, App

Sequence 608 Sequence 716 Sequence 115 Sequence 124 Sequence 785

Sequence 317, A Sequence 617, A Sequence 1831, Sequence 1869, A Sequence 629, A Sequence 627, A Sequence 627, A Sequence 630, A Sequence 630, A Sequence 630, A Sequence 630, A Sequence 131, Ap Sequence 131, Ap

OM nucleic

Run on:

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Sequence 6, Application US/10085906
; Publication No. US20030054371A1
; Sequence 6, Application US/10085906
; Publication No. US20030054371A1
; GENERAL INFORMATION:
    APPLICANT: Wing, Vincent
; APPLICANT: Wing, Vincent
; APPLICANT: Wing, Paul
; APPLICANT: Wing, Paul
; APPLICANT: Gray, Gary, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20; DB 14; Length 30;
Pred. No. 21;
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US-10-098-263B-42093

US-10-098-263B-60871

US-10-098-263B-115355

US-10-098-263B-115355

US-09-263-959-785

US-09-957-997-785

US-09-957-997-785

US-10-091-281-317

US-10-091-281-317

US-10-032-585-188

US-09-263-959-659

US-09-263-959-659

US-09-263-959-650

US-09-263-959-933

US-09-263-959-933

US-09-263-959-786

US-09-263-959-786

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US-09-263-959-786
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US-09-866-108-66
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US-10-224-005-6/c
; Sequence 6, Application US/10224005
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nes 20; Conservative
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US-10-085-906-6
     Query Match
Best Local S:
Matches 20
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Sequence 126, App
Sequence 58, App1
Sequence 1704, Ap
Sequence 1268, Ap
Sequence 77, App1
Sequence 77, App1
Sequence 77, App1
Sequence 77, App1
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Sequence 6, Appli
Sequence 167, Appl
Sequence 2, Appli
Sequence 1, Appli
Sequence 18, Appli
Sequence 18, Appli
                                                                                                             2003, 11:39:49; Search time 626.131 Seconds (without alignments) 10825.622 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_MB* PUB. seq:*
3: /cgn2_6/ptodata/1/pubpna/NSO6_NEW PUB. seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_NEW PUB. seq:*
5: /cgn2_6/ptodata/1/pubpna/US06_NEW PUB. seq:*
6: /cgn2_6/ptodata/1/pubpna/US08_NEW PUB. seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW PUB. seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB. seq:*
9: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB. seq:*
10: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB. seq:*
11: /cgn2_6/ptodata/1/pubpna/US09_NEW PUB. seq:*
11: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB. seq:*
12: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB. seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB. seq:*
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16: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB. seq:*
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17: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB. seq:*
18: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB. seq:*
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11: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB. seq:*
12: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB. seq:*
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               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-898-556A-85
US-10-353-150-77
US-10-098-263B-41465
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US-10-224-005-6

US-10-224-005-6

US-09-955-462A-1

US-09-955-462A-1

US-09-907-907A-51

US-09-907-907A-51

US-10-085-906-147

US-10-085-906-126

US-09-780-929-58

US-10-032-585-1704

US-10-033-700-1268
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                                                                                                                                                                                                                                                                                                        2169961 seqs, 1634102185 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Listing first 45 summaries
                                                                                 nucleic search, using sw model
                                                                                                                                                                                                                                                    OLIGO_NUC
Gapop_60.0 , Gapext 60.0
                                                                                                                                                                                 US-10-005-337A-2
2074
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                                                                                                                November 14,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            000041048884410888
                                                                                                                                                                                                                                                                                                                                                                                                        seq length: 0
seq length: 50
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Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
118
118
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Minimum DB Maximum DB

Database

Result

Word size

Searched:

Sequence:

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Gaps

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Gaps

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TITLE OF INVENTION: Compositions and Methods for Reproducing and Modulating Mammalian.

FILE REPERENCE: 601-1-109N
CURRENT APPLICATION NUMBER: US/09/955,462A
CURRENT APPLICATION NUMBER: US 60/233,682
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09955462A
Patent No. US20020150913A1
GENERAL INFORMATION:
APPLICANT: Wilusz, Carol
APPLICANT: Wilusz, Carol
APPLICANT: Gao, Min
APPLICANT: Messenger RNA Decapping
FILE REFERENCE: 601-1-109N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18, Application US/09439429
Publication No. US20030083275A1
GENERAL INFORMATION:
APPLICANT: Power, Christopher
APPLICANT: Mayne, Michael B.
TITLE OF INVENTION: ANTIFENSE OLIGODEOXYNUCLEOTIDES REGULATING EXPRESSION
TITLE OF INVENTION: OF TNF ALPHA
FILE REFERENCE: 3045.00002
CURRENT APPLICATION NUMBER: US/09/439,429
CURRENT FILING DATE: 1999-11-15
FRIOR APPLICATION NUMBER: 60/062,718
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100.0%; Pred. No. 2.3e+02;
live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , OTHER INFORMATION: described in specification page 28 US-09-955-462A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
0.9%; Score 18; DB 10; 1
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/955,462A CURRENT FILING DATE: 2002-04-30 PRIOR APPLICATION NUMBER: US 60/233,682 PRIOR FILING DATE: 2000-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        380 AAATAAATAAATAAA 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     380 AAATAAATAAATAAA 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37 AAATAAATAAATAAA 20
                                                                                                                                                                                                                                                                                                                          TYPE: RNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 18; Conservative
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US-09-439-429-18
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                                                                                                                                                                                                                                                                  SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 167, Application US/10224005
Sequence 167, Application US/10224005
Publication No. US20030143732A1
Sequence 167, Application No. US20030143732A1
APPLICANT: Ncharion:
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: Rosnaugh, Kachy
TITLE OF INVENTION: Gene Expression Using Short Interfering RNA
TITLE OF INVENTION: Gene Expression Using Short Interfering RNA
TITLE OF INVENTION: Gene Expression Using Short Interfering RNA
CURRENT APPLICATION NUMBER: US/10/224,005
CURRENT FILING DATE: 2002-08-20
PRIOR PILING DATE: 2001-08-28
NUMBER OF SEQ 1D NOS: 347
SOFTWARE: PatentIn version 3.0
                                                                                          APPLICANT: McSwiggen, James
APPLICANT: Fornaugh, Kathy
TITLE OF INVENTION: Ranaged, Mathy
TITLE OF INVENTION: RANA Interference Mediated Inhibition of Adenosine Al Receptor (AL
TITLE OF INVENTION: Gene Expression Using Short Interfering RNA
TITLE OF INVENTION: Gene Expression Using Short Interfering RNA
CURRENT ENERRENCE: 900/041 (MBHB01-1110-A)
CURRENT APPLICATION NUMBER: US 60/315,315
PRIOR FILING DATE: 2001-08-28
NUMBER OF SEQ ID NOS: 347
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
LENGTH: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE: OTHER INFORMATION: Description of Artificial Sequence: sinA antisense region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18; DB 12; Length 19;
Pred. No. 2.2e+02;
5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , OTHER INFORMATION: Description of Artificial Sequence: US-10-224-005-6
                                                                  APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09955462A
Patent No. US20020150913A1
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Best Local Similarity 72.2%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
              Publication No. US20030143732A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 cuccaeceauuccuucca
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APPLICANT: Wilusz, Jeffrey
APPLICANT: Wilusz, Carol
APPLICANT: Gao, Min
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
US-09-955-462A-2/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 167
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: RNA
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Gaps

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Sequence 126, Application US/10085906

Publication No. US20030054371A1

GENERAL INFORMATION:

APPLICANT: Wu, Paul

APPLICANT: Wu, Paul

APPLICANT: GENY GAL

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: GONDER: US/10/085,906

CURRENT FILING DATE: 2002-27

PRIOR APPLICATION NUMBER: US 60/126,215

PRIOR FILING DATE: 2000-03-24

PRIOR FILING DATE: 2000-03-24

PRIOR FILING DATE: 2000-03-24

NUMBER OF SEQ ID NOS: 545

COSTUMARE FASTESEQ FOR WINDOWS Version 4.0
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Patent No. US20020151693A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc
APPLICANT: Breaker, Ronald
APPLICANT: Beigelman, Leo
TITLE REPERENCE: Medico 84-4 (500/001)
FILE REPERENCE: Medico 84-4 (500/001)
CURRENT APPLICATION NUMBER: US/09/780,929
CURRENT FILING DATE: 2001-02-08
                                                                                                                                                                                     Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 34;
                                                                                                                                                                                ilarity 100.0%; Score 16; DB 14; 3
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.8%; Score 16; DB 14; I
100.0%; Pred. No. 2.4e+03;
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          SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2000-02-08
NUMBER OF SEQ ID NOS: 126
SEQ ID NO 58
LENGTH: 40
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 16; Conservative
                                                                             TYPE: DNA
CRGANISM: Homo sapiens
US-10-085-906-147
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Best Local Similarity
Matches 16; Conserva
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US-09-780-929-58
                               SEQ ID NO 147
LENGTH: 28
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APPLICANT: Fisher, Paul B.

APPLICANT: Leszcyniecka, Magdalena
TITLE OF INVENTION: GENES DISPLAYING ENHANCED EXPRESSION DURING CELLULAR SENESCENCE
TITLE OF INVENTION: TERMINAL CELL DIFFERENTIATION AND USES THEREOF
FILE REFERENCE: A34584-A-PCT-USA (070050.1664)
CURRENT APPLICATION NUMBER: US/09/907,907A
PRIOR APPLICATION NUMBER: 2001-07-16
PRIOR APPLICATION NUMBER: 1999-02-02
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FASTESEQ FOR Windows Version 4.0
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FUBLICALION O. US2000054371A1

SEQUENCE 147, Application US/10085906

FUBLICALION O. US2000054371A1

SEQUENCE INFORMATION:

APPLICANT: Wing, Vincent

APPLICANT: Wing, Paul

TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF

TITLE OF INVENTION: UNMBER: US 60/126,215

FILE REPRENCE SONO-32-37

CURRENT FILING DATE: 1999-03-22

FRIOR FILING DATE: 2000-03-24

FRIOR FILING DATE: 2000-03-24

FRIOR APPLICATION NUMBER: PCT/USO0/07938

FRIOR FILING DATE: 2000-03-24

FRIOR FILING DATE: 2000-03-24
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0.8%; Score 17; DB 11; L
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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PRIOR FILING DATE: 1997-10-22
PRIOR APPLICATION NUMBER: 09/176,862
PRIOR FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 51, Application US/09907907A Publication No. US20030099660A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               381 AATAATAAATAAA 397
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                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: RNA
CORGANISM: Homo sapiens
US-09-907-907A-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-907-907A-51/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 51
LENGTH: 34
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; Sequence 85, Application US/08898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
; FILE REPERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 85
; LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.7%; Score 15; DB 11; Length 20; Best Local Similarity 100.0%; Pred. No. 7.6e+03; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 20;
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0.7%; Score 15; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                   APPLICANT: Proll, Sean
APPLICANT: Proper, Bryan
APPLICANT: Paeper, Bryan
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF INVENTION: GENOMIC DELETIONS
FILE REPERRICE: 240083.515
CURRENT APPLICATION NUMBER: US/09/918,686
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 77
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Antisense Oligonucleotide US-09-898-556A-85
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                                                                       Sequence 77, Application US/09918686
Patent No. US20020076720A1
GENERAL INFORMATION:
APPLICANT: Brunkow, Mary
APPLICANT: Proll, Sean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 77, Application US/10353150
Publication No. US20030157543A1
GENERAL INFORMATION:
APPLICANT: Brunkow, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1234 TGTTGGGATTACAGG 1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1237 TGGGATTACAGGTGT 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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; OTHER INFORMATION: PCR primer
US-09-918-686-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TGGGATTACAGGTGT 16
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US-10-353-150-77
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US-10-238-700-1268/C
US-10-238-700-1268, Application US/10238700
; Sequence 1268, Application US/10238700
; Sequence 1268, Application No. US20030153521A1
; GENERAL INFORMATION:
    APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Rocaviggen, James
; TILE OF INVENTION: NUCleic Acid Treatment of Diseases or Conditions Related to Level
; FILE REFERENCE: 400/057 (MBHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR FILING DATE: 2002-09-18
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1268
; IENGTH: 17
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-780-929-58
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APPLICANT: Terry, Roemer D.
APPLICANT: Charles, Boone
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT PILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1704
LENGTH: 43
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                                                                               Length 40;
                                                                                                                            0; Indels
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                                                                          Query Match 0.8%; Score 16; DB 10;
Best Local Similarity 68.8%; Pred. No. 2.4e+03;
Matches 11; Conservative 5; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                       Sequence 1704, Application US/10032585 Publication No. US20030180953A1 GENERAL INFORMATION:
                                                                                                                                                                           1059 GCATTTGAGAACTTCA 1074
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                        US-10-032-585-1704/c
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; TITLE OF INVENTION: GENOMIC DELETIONS
; FILE REFERENCE: 240083.515C1
; CURRENT APPLICATION NUMBER: U8/10/353,150
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSEQ for Windows Version 4.0
; TYPE: DNA
; OTHER INFORMATION: PCR primer
US-10-353-150-77

Query Match
Best Local Similarity 100.0%; Pred. No. 7,6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0;

Qy 1237 TGGGATTACAGGTGT 1251

Db 2 TGGGATTACAGGTGT 16

Search Completed: November 14, 2003, 19:28:16
Job time: 628.131 secs
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Result
                                                                          November 14, 2003, 03:50:47; Search time 8568.5 Seconds (without alignments) 11258.085 Million cell updates/sec
                                                                                                                                US-10-005-337A-1
2358
1 ggatcctttcatgtttaaca......caggtcggaggccaccatgg 2358
                                                                                                                                                                                                                                                           5777422
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                             2888711 segs, 20454813386 residues
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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						ALIGNMENTS		
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VERSION	NOI	AX4	<u>.</u>	1 61:21	9014	02		
SOURCE	(E)	Mus	mus	lus (house		mouse)		
ORC	ORGANISM	Mus	masca	culus				
		Euk	Eukaryota Mammalia;	; Metazos Eutheris		Chordata; Cran Rodentia; Sciu	Craniata, Vertebrata, Eu Sciurognathi, Muridae, M	Euteleostomi; Murinae; Mus.
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JOURNAL Patent: WO 0246220-A 1 13-JUN-2002; Aventis Pharma S.A. (FR) ; The Regents of The University of California at San Diego (US) ; Benoit, Patrick (FR) Location/Qualifiers 1. 2358 3. 1. 2358 1. 0. 12358 1. 0. 12358 1. 0. 12358   mol_type="genomic DNA"   Abaref="taxon:10090"     Abaref="taxon:10090"   Abaref="taxon:10090"     ORIGIN	Ouery Match 100.0%; Score 2358; DB 6; Length 2358; Best Local Similarity 100.0%; Pred. No. 0; Matches 2358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy 1 GGATCCTTCATGTTAACAATATCAACCCTAACCCAAGGGGAACAGCCTGCCT	61 GGCTTTGCCACCCATGAATACTTCCTAGTCCATTTGTGAAACTCAGCCCATCCG 12	Db 121 ACACTTCTGCAAGCCCCATCCTCTACAAGGTGCTCATTGGGAATTTCCTGGAGCTTCTCT 180  Qy 181 TTCAGGATCAGCCTGATTCTAGGGCAGCAGTTCTCAACCTGGGGCCTCGACCCCTTTGG 240  Db 181 TTCAGGATCAGCCTGATTCTAGGGCAGCAGTTCTCAACCTGGGGCCTCGACCCTTTGG 240	241 GGGAATCAAACGACCCTTACAGGGGTCACATATCATCTATCCTATATGTCAGGTATTTA 30 [	Db   301 CATTACGATTCGTAACAGTAGCAAATTACAGGTATGAAATGACAATGAAATATTTAT 360	Qy         421 GGGAAAGGTTTGGGAAAAGCCTTTCTGTCCATTCTTCAAAGTGATGTGTTCACA 480           Db         421 GGGAAAGGTTTGGGGAAAGCCTTTCTGTCCATTCTTCAAAGTGATGTGTTCACA 480           Qy         481 GAAAGCCTTTCAGTGCGTCTTTGTGAGTAAGTCTGAGTAGGAACTGTATGTA	541 CAGATCTGCTTCTTATGGTGGAGCCAAGACGCATCGTGGTGGAGCGAAGCGTCACCT  541 CAGATCTGCTTCTTATGGTGAGCCAAGACGCATCGTGGGTGG		721 AAGACTGCTCAGCGCCCAGAGTCCTTCCTCAAAGGAAAGGTCTCAACTCTCAGCCCCC 7	Qy         781         TTAGCTCTGAGTCAGGCCTGGAACAACAGCCACAGGAATGAGAAAAGCTGCCATAGCTG         840           Db         781         TTAGCTCTGAGTCAGGCCTGGAACAACGGCCACAGGAATGAGAAAAGCTGCCATAGCTG         840           Qy         841         CTTGTCACTTCAAGAGGTCAAAGAAATAGTGTTAACCATGAAAACGAGAACAGAGGGAGCCAACAG         900

AUTHORS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y. Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hadez, N., Hagopian, D., Hagos, E., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Jones, C., Macdonald, P., Major, J., Manning, J., Mathaws, C., McCarthy, M., Mellad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Minova, T., Mlenga, V., Murphy, T., Naylor, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Spencer, B., Stange-Thonann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zahnoun, J., Zembek, L., Zimmer, A. and Zody, M. Jourited (11-JUW-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 11, 2030 thates Street, Cambridge, MA 02141, USA On Jun 11, 2030 this sequence version replaced gi:31455706. All repeats were identified using RepeatMasker: Smit, A. F. A. Green, P. (1996-1997) http://ftp.pageneer.med.	Center: Whitehead Institute/ MIT Center for Genome Research Center: Ode: WIBR Who site: http://www-seq.wi.mit.edu Contact: sequence_ubmissions@genome.wi.mit.edu Contact: sequence_ubmissions@genome.wi.mit.edu Contact: Droject Information Center project name: 211_P_24  * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.  * This sequence will be preserved.  * T	
0y         1981 ACAGGCAGCTGCCCTGGCTTCCCGATACGTGGGATGACTGCCATTGCTGAGCGGTGTG         2040           1981 ACAGGCAGCTGCCCTCGCTTCCCGATACGTGGGATGACTCGCATTGCTGAGCGGTGTG         2040           0y         2041 GTCACTGCCCAAAGGAATGACCCTCTCCAATTCTTCCTGATTCGCATACGCGGCCGG         2100           0y         2041 GTCACTGCCAAAGGAATGACCCTCTCACATTTCTTCCTGATTCGCATACGCCGCGCGCG	SULT 2 119234 CUS CUS FINITION CESSION ESSION WESSION WCE ORGANISM TITLE JOURNAL FERENCE AUTHORS	Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Scaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Triglio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Viel,R., Vo,A., Wilson,B., Wu,X., Myman,D., Ye,W.J., Young,G., TITLE Direct Submission JOURNAL Submitted (25-APR-2022) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  REFERENCE 3 (bases 1 to 142902)

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Direct Submission
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Allen, C. Allen, H. Alabrooks, S. Amin, A. Agguiano, D., Anyalabechi, V. Angeniano, D., Anyalabechi, V. Bandra, J. Blankenburg, K. Blyth, P. Brown, M. Bladari, J. Blankenburg, K. Blyth, P. Brown, M. Bladari, J. Blankenburg, K. Blyth, P. Brown, M. Cenera, D. Chavez, D., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Claderon, E., Davila, M., Cree, M. Divala, M., Cree, D. Berano, C., Coyla, D. Din, M., Cree, M. Divala, B., Eaves, Clayelado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., J. Deramo, C., Ding, Y., Dinh, H., Divya, K., J. Deramo, C., Ding, Y., Dinh, H., Divya, K., J. Deramo, C., Ding, Y., Dinh, H., Divya, K., J. Deramo, C., Ding, Y., Dinh, H., Divya, K., J. Deramo, C., Ding, Y., Dinh, H., Divya, K., J. Deramo, C., Ding, Y., Dinh, H., Divya, K., J. Deramo, C., Ding, Y., Dinh, H., Divya, K., J. Deramo, C., Ding, Y., Dinh, H., Divya, K., J. Deramo, C., Ding, Y., Dinh, H., Divya, K., J. Deramo, C., Ding, Y., Dinh, H., Divya, R., Dinh, J., Divya, K., J. Peraser, C., M., Gabisi, A., Gante, R., Garce, H., Garce, H., Hardan, S., Handan, S.L., Handaro, C., Hamilton, K., Hardaro, S., Kelly, S., Kally, S., Moleod, M., Levan, J., Levan, J., Levan, J., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Donason, J., Donason, R., Mangum, B., Mannoud, M., Marlor, M., Marcin, K., Martin, R., Martin, M., Mahnoud, M., Mannoud, M., M
                                                     AC105469 229640 bp DNA linear HTG 15-NOV-2002 Rattus norvegicus clone CH230-140118, WORKING DRAFT SEQUENCE, 9
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Submitted (09-JAN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 229640)
                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                          AC105469.4 GI:25007338
HTG; HTGS PHASE1; HTGS DRAFT; HTGS FULLTOP.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat Genome Sequencing Consortium.
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2 (bases 1 to 229640)
Worley, K.C.
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                                                                                                                        unordered pieces.
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JOURNAL
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
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                      AC105469
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Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:23101653.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.imc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "working draft' sequence It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project Information
Center project name: GNAG
Center clone name: CH230-140118
Center clone name: CH230-140118
Center clone name: CH230-140118
Center clone name: CH230-140118
Assembly program: Phrap; version 0.990329
Consensus quality: 217436 bases at least Q40
Consensus quality: 21866 bases at least Q20
Consensus quality: 21866 bases at least Q20
Estimated insert size: 214300; sum-of-contigs estimation
Quality coverage: 10x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Baylor College of Medicine
Center code: BCM
Center tode: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141996 CTCCCTCTTGGGCTTCCCAGACACTAAGTCTGGAATGAAATTCACCTGCCTCTGAATTG
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L Submitted (14-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 14, 2002 this sequence version replaced gi:22855482.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.ed/projects/rata). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Mithin each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole contigs within a contig-scaffold that consist entirely of whole
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Direct Submission
Submitted (11-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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Rat Genome Sequencing Consortium.
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Web site: http://www.hgsc.bcm.tmc.edu/

Contact: hgsc-help@bcm.tmc.edu

Center: Baylor College of Medicine

COMMENT

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26878 CTCAAGAGCAAAGCTTTTGGCCTTGTTTGGTTTTGGTTTAGGAATAGAACA----- 26928
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                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                              Assembly program: Phrap; version 0.990329
Consensus quality: 222569 bases at least Q40
Consensus quality: 228638 bases at least Q30
Consensus quality: 229477 bases at least Q20
Estimated insert size: 233018; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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838 bp DNA linear STS 31-MAY-2003 CZECHII/Ei Mus musculus STS genomic, sequence

BV062893 S212E60252FC3.T0 CZECHII/ tagged site. BV062893 BV062893.1 GI:31178688

DEFINITION ACCESSION VERSION

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                                                                                                                                                                                                                                                                                                               7320 Charles Street, Cambridge, MA 02141, USA
Tel: 6172521477
Fax: 6172580903
Email: kersli@genome.wi.mit.edu
Primer A: None
Primer B: None
Protocol:
WGS-discovery: Paired-end low-coverage whole genome shotgun reads
were generated from 12981/svImJ, C3H/HeJ, and BALB/CBJO. The WGS
detection was carried out by SSAHA-SNP. 225,000 reads were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 annotated as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J and the strain from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%.

Location/Qualifiers
                                                             Wade, C.M., Kulbokas, E.J. III, Kirby, A.W., Zody, M.C., Mullikin, J.C.,
Lander, E.S., Lindblad-Toh, K. and Daly, M.J.
The mosaic structure of variation in the laboratory mouse genome
Nature 420 (6915), 574-578 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481
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                                                                                                                                                                                                                                          Contact: Kerstin Lindblad-Toh
Whitehead Institute for Biomedical Research, Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.1%; Score 804.8; DB 11; Length 838; 98.9%; Pred. No. 5.2e-224; ive 0; Mismatches 7; Indels 2;
  Craniata, Vertebrata, E
Sciurognathi, Muridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/map="+ 19 27-787 35750684-35751444"
/clone lib="CZECHII/Ei"
-1...5838 231 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="CZECHII/Ei"
Chordata; (Rodentia; !
Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 838)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 98.9
Matches 831; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 665) Wade, C.M.; Kulbokas, E.J. III, Kirby, A.W., Zody, M.C., Mullikin, J.C., Lander, E.S., Lindblad-Toh, K. and Daly, M.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1781 TCTCCTTCCCCTCGGGCTGATTATCCCCAGAAATAGGATGTCCCAAAGCAACACTTCCCA
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S212RF0369FP7.TO CZECHII/Ei Mus musculus STS genomic, sequence
tagged site.
BV076484
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                                                                                                                                                                                  Length 723;
                                                                                                                                                                                                                                               Indels
                                                                                                                                                                           Score 646.2; DB 10;
Pred. No. 1.5e-177;
0; Mismatches 13;
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             /db_xref="GI:19110907"
/translation="M"
185 c 180 g
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Mus musculus
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Best Local Similarity 97.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROD 10-OCT-2002
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AF478692.1 GI:19110906
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TGAGTCTCCAGCCTCAGACGCACATTTTTCTCGGGCTCTCTTAAGCTTTTCCCACAGCAT
                                                                                                                                                                                                                                                                                                                                                                                                   300 TCTGTGCATCACTTCGGCCCGTTTTGGGGTAGATCCTCTGATTAGCCTTCAGATTTAGAA
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/product="cardiac ankyrin repeat protein"
/protein_id="AAL85342.1"
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/mol_type="genomic DNA"
/strain="FVB"
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Aventis Pharma S.A. (FR) ; The Regents of The University
California at San Diego (US) ; Benoit, Patrick (FR)
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                     Tel: 6172821477
Tel: 6172821477
Tel: 6172821477
Tel: 6172821477
Email: kersli@genome.wi.mit.edu
Primer A: None
Primer B: None
STS size: 655
Protocol:
WGS-discovery: Paired-end low-coverage whole genome shotgun reads were generated from 12931/SvImJ, C31/HeJ, and BALB/cByJ. The WGS reads were placed uniquely on the MGSC3180000 was carried out by SSAHA-SNP. 225,000 reads were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     annotated as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J as STSs and 81,000 sNPs were annotated with alleles from C57BL/6J and the strain from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%.
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structure of variation in the laboratory mouse genome (6915), 574-578 (2002)
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/ Organisma="Mus musculus"
/ mol type="genomic DNA"
/ strain="CZECHII/Ei"
/ db xref="taxon:10090"
/ map=" - 19 22-610 35751955-35751368"
/ clone_lib="CZECHII/Ei"
                                                                                                                                                                         for Biomedical Research,
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Pred. No. 8.3e-176;
0; Mismatches 8;
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al Similarity .98.6%;
656; Conservative
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Best Local Similarity
Matches 656; Conserv
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                                                                                                                   TITAGC-CCAGACATCACTCCAAAGAATTCCAAACAGATATAGACAAGTGCCTTTAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                      TTACTTCGGTTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATATAAAGCTGACCG
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                                                                  GCATTACTGAATGCTTTCAATTTCTCCTAATGCTGGTACGATGGCATGTCACAGGGCCAT
                                                                                                                                                                                                            TITAGCTGCAGACATCACTCCAGAGAATTCCAAACAGATAGAGACAAGTGGCACCCAGAC
                                                                                                                                                                                                                                                              CCATCTCCTTCCCCTCGGGCTGATTATCCCCAGAAATAGGATGTCCCAAAGCAACACTTC
                                                                                                                                                                                                                                                                              CCAGCCAACTGGAGTGCTGATAAGTCCAGTTATCAGAAAGATATGGCTGTAAGTGTGATG
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                                                   TCTCTCTGTGCATCACTTCGGCCCGTTTTGGGGT--AGATCCTCTGATTAGCCTTCAGAT
                                                                                                      TTAGAACACGGTGAGCCTGTGGTGCACTAATTATGGCCAGTGACACCATAGAGTCAAAGT
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                           22;
 Length 2074;
                           Indels
Score 367.8; DB 9;
Pred. No. 5.9e-96;
0; Mismatches 162;
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ALS90622.7 GI:14270159
HTG; CARP; ribonuclease P
Homo sapiens (human)
Homo sapiens
Query Match
Best Local Similarity 76.4%;
Matches 597; Conservative
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Submitted (26-FEB-1999) Second Department of Internal Medicine,
Gunma University School of Medicine, 3-39-15 Showa-machi, Maebashi
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2074)
Aihara,Y., Kurabayashi,M., Tanaka,T., Sekiguchi,K., Tomaru,K.,
Kanai,H., Takeda,S. and Nagai,R.
Human CVARP 5'-flanking region
Unpublished
2 (bases 1 to 2074)
Aihara,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="cardiovascular-specific cardiac ankyrin repeat
protein"
                                                                                                              CCTGATTCGCATACGCCGCGG-----CCAGCTTGTCATCTCCCTTTGGGCTTCCCAGAC
                                                                                                                               TGACTTGGCTTCCCAGGCTGGAAGATTATCTCACCCAGGCCTAGCTATATAA-CGGGCTG
                                                            2016 ATGACTCGCATTGCTGAGCGGTGTCGCCAAAGGAATGACCCTCTCACATTTCTT
                                                                              1938 TIACTICGGTTCCCAGGTTGGAAGATTATCTCACCGGGCCCCAGCTATATAAGCTGACCG
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            AGAGCAGCGATGTGGTGCAATATTAACAGGCAGCTGTCCCC
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/organism="Homo sapiens"
/mol type="genomic DNA"
/db_Xref="taxon:9606"
1. 1832
/note="5'-flanking region"
1833
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1833. .>2074
/gene="CVARP"
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1833. .2074
/gene="CVARP"
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371-8511, Japan
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/trānslation="MAVFADLDLRAGSDLKALRGLVETAAHLGYSVVAINHIVDFKEK
KQEIEKPVAVSELFTTLPIVQGKSRPIKILTRLTIIVSDPSHCNVLRATSSRARLYDV
VAVFPKTEKLFHIACTHLDVDLVCITVTEKLPFYFKRPPINVAIDRGLAFELVYSPAI
                                                                                                                                                                                                        KDSTWRRYTISSALNIMQICKGKNVIISSAAERPLEIRGPYDVANLGLLFGLSESDAK
AAVSTNCRAALLHGETRKTAFGIISTVKKPRPSEGDEDCLPASKKAKCEG"
                       /evidence=not_experimental
/product="bA320E15.1.1 (ribonuclease P (30kD) (RPP30))"
/protein id="AAC70100.1"
/db_xref="G1:15717970"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5722. .6237
/note="L2 repeat: matches 1200. .1808 of consensus"
6884. .7196
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                                                                                                                                                                                                                                                                                                            .2749 of consensus"
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//Octe="MIR repeat: matches 76. 212 of consensus"

10798. 11076

//Octe="Alux repeat: matches 1. 291 of consensus"

11086. 11219
                                                                                                                                                                                                                                                          689. .800
/note="MTR_repeat: matches 30. .132 of consensus"
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/note="HY1 repeat: matches 16. .112 of consensus"
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note="match: ESTs: Em:AW939965"
evidence=not_experimental
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/note="2 copies 81 mer 81% conserved"
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/note="AluSx repeat: matches 7.
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/note="AluSx repeat: matches 1.
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13755. .13817
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/note="L2 repeat: matches 2423.
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1926. .2208
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'note="match: GSS: Em:B92129"
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/gene="bA320F15.1"
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/note="HY1 re
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/gene="ba320F15.1"
/groduct="ba320F15.1"
/product="ba320F15.1.1 (ribonuclease P (30kD) (RPP30))"
/note="match: cDNAs: Em:U77665 Em:AK004137 Em:U95123
match: ESTS: Em:B6572689 Em:BE378859 Em:BE37893
Em:B4920575 Em:B6106820 Em:BF681617 Em:BF248001
Em:BF031745 Em:A4854455 Em:A1359795"
                                                                                                              Direct Submission

Submitted (19-SED-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On May 31, 2001 this sequence version replaced gi:14161205.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone ander. Note that the variation manotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, SNISSEROT; Tr:, TREMBL; Wp:, WORWPEP; Information on the WORMPEP database can be found at the sanger centre chromosome 10 happing Group. Further information can be found at the special centre chromosome 10 happing Group. Further information can be found at http://www.sanger.ac.uk/FGP/Chr10

RPI1-320FLS is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm

WETOR: PBACBA:
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join(391. 475_3273. 3328,3962. .4018,4428. .4502,7467. .7538,
14216. .14305,23179. .23295,23858. .23887,24284. .24321,
24717. .24796,28974. .29083)
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The true left end of clone RP11-236B18 is at 50012 in this sequence. The true right end of clone RP11-103A2 is at 100 in this
  Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
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// note="match: GSS: Em:AQ670367"
complement (1. .97)
//note="match: GSS: Em:AQ544636"
complement (1. .77)
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match: GSS: Em:AQ311708"
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mol_type="genomic DNA"
db_xref="taxon:9606"
/chromosome="10"
/clone="RP11-320F15"
/clone="RP11-320F15"
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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/gene="bA320F15.1"
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Novel target genes for diseases of the heart
Patent: WO 0192567-A 19 06-DEC-2001;
Medigene AG (DE)
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
_378 c 460 g 471
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join (23179: .22295, 23858. .23887, 24284. .24321,24717. .24796,
28974. .29072, 30647. .30748,31596. .31680,33706. .34469)
/gene="bA320F15.1"
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complement(join(24284, .24321,24724, .24796,28974, .29240))
/note="match: STS: Em:G24365"
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                                                                                                                                                                                                                                                                                            /product="pA320F15.1.3 (putative isoform 3)"
/note="match: ESTs: Em:BE567341 Em:A1292002 Em:BF684192
Em:BF435407 Em:A1740881 Em:AA651912 Em:BF438915"
/evidenct_experimental
/gene="bA320F15.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="L1MA2 repeat: matches 5888. .6302 of consensus"
                                                                   "note="AluSx repeat: matches 45. .304 of consensus"
19198. .19363
"note="LiME repeat: matches 5272. .5435 of consensus"
19489. .19928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50106 AAAGTGCATTACTGAATGCTTTCAATTTCTTATAATGATGGTAGGTGGGCATGTCATGGG
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                                                                                                                                      /note="MLTIC repeat: matches 5. .478 of consensus" 21838. .2258 //note="L2 repeat: matches 2109. .2669 of consensus" 22440. .22946 //gene="bA320F15.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8442. .28516
note="L2 repeat: matches 2636. .2710 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .133 of consensus'
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25321. .25458
Conte="FLAM C repeat: matches 1.
complement (25417. .25863)
/note="match: GSS: Em:AQ712354"
26204. .26603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 14.7%; Score 347.6; DB 9; Best Local Similarity 78.2%; Pred. No. 7e-90; Matches 521; Conservative 0; Mismatches 129;
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.7709. .17972
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.7236. .17755
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gene="bA320F15.1"
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CLEGHLAIVEKLAMGAQAQIEFRDMLESTAHTHAA
CLEGHLAIVEKLAMGAQAQIEFRDMLESTAHTHAA
CLEGHLAIVEKLAMGAQAQIEFRDMLESTAHTHAA
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                    Direct Submission
Submitted (05-JAN-1995) W. Chu, Hoffmann-La Roche, 340 Kingsland
Street, Dept. of Inflammation/Autoimmune Disease, Hoffmann-La
Roche, Nutley, M 0710, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2225 CCAGCCCTAGCTATATAA-CGGGCTGGTGTGGAGGGGCTCCACAGGGCCAGTTCCAGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="cytokine-inducible expression"
nuclear protein from human endothelial cells J. Biol. Chem. 270 (17), 10236-10245 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                             94. .98
/note="nuclear localization signal"
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ches 34;
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Pred. No. 6.9e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152. .283
/note="ankyrin-like repeats"
                                                                                                                                                                                                                        1. .1901
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/db xref="taxon:9606"
/chromosome="10"
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                                                                                                                                                                                                                                                                                                                                          /cell_type="endothelial"
/tissue_type="skin"
/clone_lib="HDMEC_cDNA"
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                                                                                                                                                                                                                                                                                                                             /clone="C-193"
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Best Local Similarity 82.6%;
Matches 171; Conservative (
                                                                              (bases 1 to 1901)
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                    J. Biol. 95247734
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Chu, W.
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VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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TITLE
JOURNAL
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                    JOURNAL
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                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1. (Dasas 1 to 1901)

Sakurada,K., Kuga,T., Sekine,S., Nakamura,Y. and Sugan,S.
Shear stress-responsive DNAs

Shear stress-responsive DNAs

LARRON KOGYO CO LID, HIGOSHI NOJIMA, HAJIME YOSHISUE, MASAYA
SUSUMU SEKINE, YUSUKE NAKAMIRA, SUMIO SUGANO
OS HOmo sapiens (human)
PN WO 0125427-A/37

PD 12-APR-2001
PR 02-OCT-2000 WO 2000JP006840
PR 01-OCT-1999 JP 99P 280976
PR HIROSHI NOJIMA, HAJIME YOSHISUE, MASAYA OBAYASHI, TOSHIO OTA, PI
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                                                                                                                                                                                                                                                                                                                                                                                                    AYAKO KAWABATA,
PI KAZUHIRIO SAKURADA, TETSURO KUGA, SUSUMU SEKINE, YUSUKE NAKAMURA,
PI KAZUHIRIO SAKURADA, TETSURO KUGA, SUSUMU SEKINE, YUSUKE NAKAMURA,
PI SUMIO SUGANO
PC C12N15/12, C07K14/435, C07K16/18, C12P21/02, C12Q1/68, A61K38/00,
PC A61K39/395,
PC A61K48/00, A61P9/10, G01N33/50, G01N33/53
PC FF KEY
FT CDS (120K)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 CCGGCCCCAGCTATATAAGCTGACCGGTGTGGAGGGCCCCAGCAGCCCAACTCCAGGGA 206
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Identification and characterization of a novel cytokine-inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAGCCCTAGCTATAA-CGGGCTGGTGTGGAGGGGGCTCCACAGGGCCCAGTTCCAGGGG
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H.sapiens mRNA for cytokine inducible nuclear protein.
X83703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata;
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Pred. No. 6.9e-26;
0; Mismatches 34
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ankyrin-like repeat; nuclear loc
Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Ci
Mammalia; Eutheria; Primates; Ci
                        GI:22639664
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ilarity 82.6%;
Conservative 0
                                                            Homo sapiens (human)
Homo sapiens
BD094076
BD094076.1 GI:23
WO 0125427-A/37.
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Matches 171;
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                                                                                                                                                                                                                                                                  degrees C for 15 seconds degrees C for 23 seconds degrees C for 30 seconds
                                                                                                                                                                                                                                        Initial incubation: 94 degrees C for 90 seconds
                                                          Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
                                                                                                                                                                                                                                                                   94 degrees C for 15
62 degrees C for 23
72 degrees C for 30
30
Perkin Elmer 9600
                                                                                                                                                                                                                                                                                                                                                          25 ng
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378 c 460 q 4
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/db_xref="taxon:9606"
                                                                                                                                                                            Primer A: GGCATTTTGAAGGCATGG
Primer B: CCAGATGGATGATCATGAAGG
STS size: 22
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.5 mM
50 mM
20 mM
8.3
                                                                                                                                                 Email: myers@shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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Annealing:
Polymerization:
                                                                                                                                                                                                                                                                                                                                                                                                     Tag Polymerase:
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1246. .1263
 1 (bases 1 to 1901)
Myers, R.M.
Unpublished (1996)
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RESULT 15 AC074094/c

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ACU/4094 160350 bp DNA linear HTG 01-SEP-2000
Homo sapiens chromosome 10 clone RP11-236B1B, WORKING DRAFT
SEQUENCE, 17 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (Bases 1 to 160350)
Waterston, R.H.
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of 1355 bp in length
unknown length
of 1655 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence of Homo sapiens clone Unpublished
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HTG; HTGS PHASE1; HTGS_DRAFT.
Homo sapiens (human)
Homo sapiens
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gap of
contig
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Waterston, R.H.
Direct Submission
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113587 GCATTACTGAATGCTTTCAATTTCTTATAATGATGGTAAGGTGGCATGTCATGGGGCCTA 113528
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                                                        187 150852: contig of 3466 bp in length 1853 150952: gap of unknown length 1953 153550: contig of 2598 bp in length 1551 153670: gap of unknown length 1651 157357: contig of 3607 bp in length 157357: gap of unknown length 1588 160350: contig of 2993 bp in length 16621007/Qualifiers
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                                               length
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note="assembly_name:Contig13"
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note="assembly_name:Contig14"
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note="assembly_name:Contig16"
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note="assembly_name:Contig17"
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                                                                                                                                                                                                                                                                                                                                       427. .7519
note="assembly_name:Contig11"
                                                                                                                                                                                                                                                                                                                                                                        620. .15286
note="assembly_name:Contig12"
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41833. .143187
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47387. .150852
note="assembly_name:Contig6"
50953. .153550
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43288. .144942
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45043. .147286
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note="assembly_name:Contig9"

ture 157365. 160350

/note="assembly_name:Contig9"

47390 a 32724 c 33135 g 45498 t
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53651. .157257
contig of 2244 bp
                                                                                                                                                                                                    1. .160350
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="10"
/clone="RP11-236B18"
                                                                                                                 153551
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Search completed: November 14, 2003, 11:17:42 Job time : 8578.5 secs

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 05-DEC-2001; 2001WO-EP15412
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(c) 1993 - 2003 Compugen Ltd
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... promover sequence derived from a portion upstream of the coding sequence of a gene for Cardiac Ankyrin Repeat Protein, for controlling the level and specificity of expression of a transgene in cardiac muscle cells

1; 48pp; English. Claim 1; Fig

The invention relates to a polynucleotide (I) comprising a fragment of a sequence upstream of the coding part of the gene for the Cardiac Ankyrin Repeat Protein (CARP). (I) is capable of inducing a specific expression in vivo of a gene operably linked to (I), in cardiac cells. (I) or a vector (IIb) comprising (I) is useful for the manufacture of a medicament intended for the treatment of cardiac insufficiency, cardiac hypertrophy and hypoxia, and for preventing rejection during cardiac transplant. An expression cassette under the control of (I) is useful for encoding a protein or RNA which is capable of activating the growth of cardiac calls. reducing or suppressing an immune response, inducing angiogenesis, correcting muscle contractility, cardiac hypertrophy, cardiac cardiac charageutic interest in vivo, by isolating (IIb) and introducing (IIb) in the cardiac tissue, under conditions so that the gene of interest is expressed. (I), the vectors and the compositions are useful in clinical, expressing cardiac pathologies. (I) is also useful for generating transgenic animals which constitute models for studying certain cardiac perhologies. (I) is also useful for generating modelucius for their activity on the regulatory sequences of the gene cenceding the CARP protein. The present sequence represents the DNA fragment upstream of the coding sequence of a mouse CARP protein. 

Seguence 2358 BP; 636 A; 567 C; 542 G; 613 T; 0 other;

120 120 180 180 240 240 300 300 360 420 420 480 480 540 900 360 9 GGGAATCAAACGACCCTTTACAGGGGTCACATATCATCTATCCTATATGTCAGGTATTA GGGAAAGGTTIGGGAAAGCCTTTCTGTCCATTCTTCATTCTTCAAGTGATGTGTCACA GGGAAAGGTTTGGGAAAAGCCTTTCTGTTCTTCATTCTTCAAAGTGATGTGTTCACA GGCTTTGCCACCATGAATACTTCCTAGTCTAGTCCGTTTGTGAAACTCAGCCCATCCCA CATTACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTAAT GATTGAAGGTCACCACAACATGAGGCCCCCCACACTGTTCTAGAGAAAAATCACCTGGGTG GATTGAAGGTCACCACAACATGAGGCCGCCACACTGTTCTAGAGAAAAATCACCTGGGTG ACACTICTGCAAGCCCCATCCTCTACAAGGTGCTCATTGGGAATTTCCTGGAGCTTCTCT TTCAGGATCAGCCTGATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGG TTCAGGATCAGCCTGATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCTTTGG GGCTTTGCCACCCATGAATACTTCCTAGTCTAGTCCGTTTGTGAAACTCAGCCCATCCCA ACACTTCTGCAAGCCCCATCCTCTACAAGGTGCTCATTGGGAATTTCCTGGAGCTTCTCT Gaps DB 24; Length 2358; . . Indels .; 0 100.0%; Score 2358; ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches Similarity Query Match Best Local Simil Matches 2358; 61 Н н 61 121 121 181 181 241 241 301 301 361 361 421 481 421

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Evans S;

Wang Y,

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The invention relates to a human type-5 recombinant adenovirus vector for achieving cardiac-restricted transcription of a gene of interest. The vector comprises inverted terminal repeat (ITR) sequences from human adeno-associated virus (AAV) type 2 (AAAI0409) and a cardiac tissue-specific promoter. In particular, the promoter is that of the cardiomycoyte-restricted cardiac ankyrin repeat protein (CARP) gene. The adenovirus vector is used for targetted gene therapy for heart disease and for evaluating gene function. Cardiac restricted transcription of a transgene in both neonatal and mature cardiac tissues can be achieved to treat inherited and acquired heart diseases. The vector is suitable for tissue-specific use in vivo and in vitro and provides cardiac restricted transcription. The present sequence
                                                                                                                                                                                                                                                                                                                                                                        represents the murine cardiac ankyrin repeat protein (CARP) promoter
                                                                                                  Human type-5 recombinant adenovirus vector used for targeted gene therapy for heart disease and evaluating gene function contains a tissue-restricted promoter and inverted terminal repeat sequences
                                                                                                                                                               Claim 8; Page 29-30; 33pp; English
                UNIV CALIFORNIA
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                                             Chien KR,
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                                                                                                                                                                                      GGCTTTGCCCACCATGAATACTTCCTAGTCTGAGTCCGTTTGTGAAACTCAGCCCATCCCA
                                                                                                                                                                                                                       GGCTTTGCCACCCATGAATACTTCCTAGTCTAGTCCGTTTGTGAAACTCAGCCCATCCCA
                                                                                                                                                                                                                                                                                                151 ACACTICIGCAAGCCCCATCCTACAAGGIGCTCATIGGGAATTICCTGGAGCTICTCT
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                                                                                                                                               ACACTTCTGCAAGCCCCATCCTCTACAAGGTGCTCATTGGGAATTTCCTGGAGCTTCTCT
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                                                                       Gaps
                                    DB 21; Length 2247;
                                                                       69; Indels 137;
                                                                                                            Seguence 2247 BP; 609 A; 549 C; 485 G; 589 T; 15 other;
                                Query Match
74.8%; Score 1763.4;
Best Local Similarity 91.2%; Pred. No. 0;
Matches 2124; Conservative 0; Mismatches
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99WO-US20730 0966600-SD86

10-SEP-1999; 11-SEP-1998;

23-MAR-2000

WO200015821-A1. Mus musculus

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The invention relates to a polynucleotide (I) comprising a fragment of a sequence upstream of the coding part of the gene for the Cardiac Ankyrin Repeat Protein (CARP). (I) is capable of inducing a specific expression in vivo of a gene operably linked to (I), in cardiac cells. (I) or a vector (IIb) comprising (I) is useful for the manufacture of a medicament in the dragment of cardiac insufficiency, cardiac hypertrophy and hypoxia, and for preventing rejection during cardiac transplant. An expression cassette under the control of (I) is useful for encoding a correcting muscle contractility, cardiac hypertrophy, cardiac or RNA which is capable of activating the growth of cardiac correcting muscle contractility, cardiac hypertrophy, cardiac correcting muscle contractility, cardiac hypertrophy, cardiac for expressing a gene of therapeutic interest in vivo, by isolating (IIb) and introducing (IIb) in the cardiac tissue, under conditions so that the gene of interest is expressed. (I) the vectors and the compositions are useful in clinical, expressing cardiac pathologies. (I) is also useful for screening cransgenic animals which constitute models for studying certain cardiac pathologies. (I) is also useful for screening molecules for their activity on the regulatory sequences of the gene concoding the CARP protein. The present sequence represents the DARP protein.
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                                            New promoter sequence derived from a portion upstream of the coding sequence of a gene for Cardiac Ankyrin Repeat Protein, for controlling the level and specificity of expression of a transgene in cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTCTCTGTGCATCACTTCGGCCCCGTTTTGGGGT--AGATCCTCTGATTAGCCTTCAGAT
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0; Mismatches 162; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2074 BP; 612 A; 469 C; 416 G; 572 T; 5 other;
                                                                                                                                                         Claim 5; Fig 2; 48pp; English.
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Matches 597; Conservative
WPI; 2002-740642/80.
                                                                                                                 muscle cells
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                                                                                                                              The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA00010-AA01310) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or polynucleotides and polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
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                                                                                                                                                                            GTGTGGAGGGCTCCACAGGGCCAGTTCCAGGGGTTCATCCACAAGAGAGAAAAAATAG
             CCTGATTCACATATTCAGCAGGGTTAGCTTGTCCTCCCCTCCTCTTCAGCTTCCCAGAC
                                                                             ACTGAGTCTGGAATGAAATTCACCTGCCTCTGAGTTGGCTCCTAATGGGGGCGGGGAGTG
                                                                                                           TGACTTGGCTTCCCAGGCTGGAAGATTATCTCACCCAGCCCTAGCTATAA-CGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 13568; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human polynucleotide SEQ ID NO 13568.
                                                                                                                                                                                                                                                                                                                                                             AAI93508 standard; cDNA; 1988 BP.
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18-MAY-2000; 2000US-0577409.
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                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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2164 ,,

2310

Gaps

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congestive heart failure; dilative cardiomyopathy; sudden death;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypercrophic cardiomyopathy, ischaemic cardiomyopathy; rhythm disorder; heart muscle disease; conduction disorder; coronary heart disease; systemic arterial hypertension; pulmonary hypertension; endocarditis; pulmonary heart disease; valvular heart disease; pericardial disease; congenital heart disease; gene therapy; syncope; transgenic animal; expressed sequence tag; EST; clone X83703; CAA58676 protein; ds.
                                                                                                                                             87 gridecrecraargesestesesasierracricesricecassirasaarrarereae
                                                                                                                                                                             CCAGCCCTAGCTATATAA-CGGGCTGGTGTGTGGAGGGGCTCCACAGGGCCAGTTCCAGGGG
                                                                                                           2165 ATTGGCCACTGGTGGGGGAGGGGTGTGACTTGGCTTCCCAGGCTGGAAGATTATCTCAC
                                                                             27 rececrecererreagerreceagacacrearrersgaareaaarreacerseerea
Pred. No. 1e-26;
; Mismatches 34; Indels
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/note= "AU-rich mRNA decay element"
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/note= "SIMC01-1 cDNA fragment"
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/note= "66268 cDNA fragment"
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1415..1423
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82.6%;
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Best Local Similarity 82.6
Matches 171; Conservative
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                                                2105 TCATCTCCCT
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                                                                                                                                                                                                                                                                                                                                                          AAD27217 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides the protein and coding sequences of a number of human shear stress response proteins. These are useful in the diagnosis, treatment and screening of vascular diseases caused by arteriosclerosis, including heart failure, post-PTCA restenosis and
obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1901 BP; 592 A; 378 C; 460 G; 471 T; 0 other;
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scification, but was obtained in electroni ftp.wipo.int/pub/published_pct_sequences.
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Sugano S;
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Nakamura Y,
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(NOJI/) NOJIMA H.
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The patent discloses novel target genes abnormally expressed in heart tissues and their corresponding proteins. The invention also relates to methods for assessing the expression level of these genes. The method is used for testing the predisposition of mammals and preferably humans for a heart disease or for an acute state of such a disease. It is also useful to treat diseases of the heart such as congestive heart failure, dilative cardiomyopathy, hypertrophic cardiomyopathy, isohaemic cardiomyopathy, property disease, rhythm and conduction disorders, syncope and sudden dath, coronary heart disease, systemic arterial hypertension, pulmonary hypertension, pulmonary hypertension, pulmonary heart disease, congenital heart disease, pericardial disease and conduction non-human mammal comprising the sequences of the invention are useful for the development for medicaments for the treatments of the control of the invention are useful for the development for medicaments for the treatments of the control of the control
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                                                                                         Identifying a subject at risk for a heart disease e.g. congestive heart failure, dilative cardiomyopathy, heart muscle disease, by quantifying the polypeptide expressed by genes abnormally expressed in heart tissue
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Gastric Antrum Mucosal Protein 18, useful for preparing a composition for healing of the injured gastrointestinal tract
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is that of a gene encoding a novel member of the murine gastrokine group, designated antrum mucosal protein 18 (AMP-18). AMP-18 was initially detected in mammalian gastric antrum mucosa by a differential screen of cDNA libraries obtained from different regions of the pig stomach. A cDNA was also isolated from a mouse library (see ABZ24660). Genomic AMP-18 DNA sequences were subsequently cloned as a prelude to the analysis of gene regulatory elements. AMP-18 protein is expressed at high levels only in the gastric antrum, and is synthesised in the lumenal surface mucosal cells. Partially purified AMP-18s from mouse and pig antrum tissue are mitogenic to confluent stomach and kidney epithelial cells in culture. This effect is inhibited
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Best Local Similarity 80.5
Matches 136; Conservative
                                                                                     Martin TE,
                                                                      (UYCH-) UNIV CHICAGO
                                                                                                    WPI; 2003-103239/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003004637-A1
       WO200278640-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-JAN-2003.
                       10-OCT-2002
                                                                                     GF,
                                                                                                                                                                                                                                                                                                                    258
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                                                                                     Toback
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                                                                                                       391 TCTAGAGCAGTGGTTCTCATCCTGTGGGCCATGAGCCCTTTGGGGGGGTTGAACGACCCT 450
                                                                                             TT-ACAGGGGTCACATATCATCTATCCTATATGTCAGGTATTTACATTACGATTCGTAAC 316
                                                              198 TCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCTTTGGGGGAATCAAACGACCCT
                                                                                                                                                                                                                                              Cellular growth stimulating protein; gastric antrum mucosal protein; gastrokine; AMP-18 protein; gastro-intestinal disorder; cell therapy; ulcer; mouse; ds.
                                               Gaps
                                               3;
                                                                                                                           317 AGTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATTG 365
                                                                                                                                        511 AGTAGCAAAATT--AGTTAGGAAGTAGGAACAAAATAACGTTATGGTTG 557
                             Length 7280;
              Seguence 7280 BP; 2131 A; 1597 C; 1606 G; 1944 T; 2 other;
                             Query Match
4.0%; Score 95; DB 25; Length 72
Best Local Similarity 80.5%; Pred. No. 1.6e-16;
Matches 136; Conservative 0; Mismatches 30; Indels
cells in the gastrointestinal tract
                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                  AAD50815 standard; DNA; 7280 BP.
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/*tag= f
/number= 3
4595..4705
/*tag= g
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4706..5607
/*tag= h
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5608..5749
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1957..3531
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3583..3672
/*tag= d
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/*tag= k
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/*tag= a
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/number= 5
5750..6444
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/*tag=
                                                                                                                                                                                                                                 Mouse pre-AMP-18 gene.
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                                                                                                                                                                                                  AAD50815;
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                                                                                                                                                                  RESULT 8
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391 reradadedergerrerearcergrededeceardadecerrredededegredadedeer 450
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                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a protein inhibitor which comprises homologous cellular growth stimulating proteins designated gastrokines. The invention also provides gastric antrum mucosal proteins designated AMP-18 which belongs to the novel group of gastrokines and nucleic acid molecules encoding such proteins. Pharmaceutical composition comprising growth stimulating peptide derived from a gastrokine protein is useful for treating gastro-intestinal disorder or diseases associated with overgrowth of gastric epithelia e.g. ulcer. The invention is useful therapy. The present sequence is mouse pre-AMP-18 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451 Trcacaddedcarartcagararccigcarcradcrarracarracarracarracaraac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198 TCTAGGGCAGCAGTTCTCAACCTGGGGCCTCGACCCCTTTGGGGGAATCAAACGACCCT
                                                                                                                                                          Protein inhibitor, useful for treating gastrointestinal disorders or diseases comprises isolated homologous cellular stimulating proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse, drug composition, food intake disorder, body weight disorder;
histamine receptor H3; anorectic, gene, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317 AGTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATTG 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          511 AGTAGCAAATT--AGTTAGGAAGTAGGAACAAATAACGTTATGGTTG 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 7280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 7280 BP; 2131 A; 1597 C; 1606 G; 1944 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.0%; Score 95; DB 25;
80.5%; Pred. No. 1.6e-16;
vative 0; Mismatches 30;
Walsh-Reitz M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse histamine receptor H3 gene.
                                                                                                                                                                                                                                                                                                       Disclosure, Fig 4; 84pp; English
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ABZ82337 standard; DNA; 18105 BP
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208828 GCAGCAGTTCCCAACGTGTGGGTCCAGATCTCTTTGGGAG-CCGAAAGGGCCTTTCACAG 208886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            324 AAATTACAGGTATGAAATAGCAATGAAATAATTTTA----TGATTGAAGGTCACCACAAC 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention provides a DNA molecule that directs neuron-specific transcription of a promoter segment in a mammalian cell. The promoter segment is from the mouse genomic Presentlin-1 gene. Transgenic non-human
                                                                                                                                                                                                                                                                                                         Sequence 659158 BP; 177521 A; 147222 C; 149414 G; 184754 T; 247 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                        204 GCAGCAGTICTCAACCTGGGGGCCTCGACCCCTTTGGGGGGAAICAAACGACCCTTTACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGTCACATATCATCTATCTATATGTCAGGTATTTACATTACGATTCGTAACAGTAGCA
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
The invention describes an isolated nucleic acid molecule encoding gene product that, when knocked out, results in a high growth (hg) phenotype. For example a nucleic acid disrupting the Socs2 gene is useful for producing an animal characterised by a hg phenotype, by inhibiting expression of Socs2 (supressor of cytokine siganling 2) gene. The nucleic acids of the invention are useful for regulating body size in mammals. gene. The nucleic acids of the invention are useful for regulating body size in mammals. gene. The nucleic acids of the invention are useful for regulating body size in mammals. This sequence represents the mouse high growth region.

Note: This sequence did not form part of the printed specification but was obtained in electronic format directly from the US patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuron-specific transcription; promoter; mouse; Presenilin-1 gene; transgenic; laboratory model; Alzheimer's disease; ss.
                                                                                                                                                                                                                                                                                                                                                      Length 659158;
                                                                                                                                                                                                                                                                                                                                                                                              42; Indels
                                                                                                                                                                                                                                                               segdata.uspto.gov/seguence.html?DocID=20020155564
                                                                                                                                                                                                                                                                                                                                                    Score 88.8; DB 25;
Pred. No. 1.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse Presentlin-1 gene sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX55300 standard; DNA; 48974 BP
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                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 74.7
Matches 139, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209007 ATGAGG 209012
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                                                                                                                                                                                                                                             office at
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                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    °;
                                                                                                                                                                                                                The invention relates to novel drug compositions for the treatment and prevention of disorders of food intake and body weight containing as the active component histamine receptor H3 protein, or DNA encoding it, or an agonist or antagonist to it. A composition of the invention has anorectic activity. Compositions containing the histamine receptor H3 protein may be used in the treatment and prevention of disorders of body weight and food intake. The present sequence represents the mouse histamine receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGACCCTTTACAGGGGTCACATATCATCTATCCTATATGTCAGGTATTTACATTACGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel gene that when downregulated or knocked-out, results in high growth phenotype, useful for regulating body size in mammals e.g. rodent, bovine and canine -
                                                                                                          receptor H3 protein and its agonists and antagonists for and prevention of body weight and food intake disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 18105;
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                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18105 BP; 3981 A; 5123 C; 4944 G; 4041 T; 16 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.8%; Score 89.2; DB 25; 79.1%; Pred. No. 1.3e-14; ative 0; Mismatches 28;
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                                                                                                                                                                           Example 1; Page 53-65; 73pp; Japanese.
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                          Suwa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse high growth region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 371 CACCACAACATGAG
                        Takahashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (REGC ) UNIV CALIFORNIA
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                                                                  WPI; 2003-221596/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 106; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2002155564-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-APR-2003
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                                                                                                            Histamine
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                                                                                                                                                                                                                                                                                                                                                                          gene
                        Kotani
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Sequence 707 BP; 205 A; 174 C; 156 G; 169 T; 3 other;
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                                                       Matches 148;
                                                                                                                           231
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                                                                                                                                                                                                                                                                            RESULT 13
ABX16390/
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                                                                                                                                                                                                                                   15385 GCTACACTCTAGATCGGTGGTTCTCAAGCTGGGGGGTCGCGACCCCTTTGGGGGGTTGGACA 15326
                                                                                                                                                                                             15325 A-CCTTTTCACAAGGGTCACATCAGAGATCCTGCATATCGATATTTATGTTATGATT 15267
                                                                                                     Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method used for evaluating the toxicity of an agent comprising determining the expression of a rat toxic response egene(8) in the test animal in response to the agent. The method is useful in drug development, particularly for conducting toxicity studies and analysis before a new drug or compound is approved for human consumption or use. The method is also useful in determining toxicological responses to a new drug. This polynucleotide sequence represents a phase-1 rat CT gene of the invention.
                                                                                                                           250
                                                                                                                                                                         310
                                                                                                                                                                                                                    370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Evaluating the toxicity of an agent, useful in drug development or in determining toxicological responses to a new drug, by determining the expression of rat toxicologically relevant genes in the test animal in
                                                                                                                           191 GCCTGATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGGGGGAATCAAA
                                                                                                                                                                       251 CGACCCTTTACAGGGGTCACATATCATCTATCCTATATGTCAGGTATTTACATTACGATT
                                                                                                                                                                                                                     CGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATTGAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                        toxicity study; rat toxic response gene; toxicological response; development; phase-1 rat CT gene; ds.
                                                                                                     Gaps
mammals containing a DNA expression cassette comprising the neuron-
specific promoter are useful as laboratory models for studying the
function of the Presenilin gene, and for studying the etiology of
                                                        Sequence 48974 BP; 12579 A; 10749 C; 11189 G; 14438 T; 19 other;
                                                                                                     1;
                                                                             Length 48974;
                                                                                                    Indels
                                                                           DB 20;
..5e-14;
les 59;
                                                                             Score 88.6; DB
Pred. No. 3.5e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 155; 388pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                    gene SEQ ID No 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SB;
                                                                                                                                                                                                                                                                                   15206 CACCATGACATGAAG 15192
                                                                                                                                                                                                                                                                                                                                                 ABT09109 standard; DNA; 707 BP
                                                                                                                                                                                                                                                                 371 CACCACACATGAGG 385
                                                                             Query Match 3.8%;
Best Local Similarity 69.2%;
Matches 135; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-2001; 2001US-264933P.
26-JUL-2001; 2001US-308161P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             response to the test agent
                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                  Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                    Phase-1 Rat CT
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat;
drug
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348
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                                                                                                                                                                                                                                                                                                                                                                                                292 ACCCCTTTGGGGGTTAAATGACCCTTTCACATATCAAATATCAAATACCTGCAG 351
                                                                                                                                                                             GAGCCATCCCTCCAGCCCCAGCCTGTTTTATGGAAGTGATTCTCAACTCATGGGTCATG
                                                                                                                                                                                                                                                                                                                                                        GTCAGGTATTTACATTACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATG
                                                                                                                                                                                                                                       GAGCTTCTCTTTCAGGATCAGCCTGATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCG
                                                                Gaps
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Note: This sequence did not form part of the printed specification but was obtained in electronic format directly from the US patent office at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes an isolated nucleic acid molecule encoding
                                                             3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene that when downregulated or knocked-out, results in h phenotype, useful for regulating body size in mammals et, bovine and canine -
      707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High growth region; high growth phenotype; Socs2; body size; supressor of cytokine signaling 2; ds; mouse.
      Length
                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -AAATAATTTTATGATTGAAGGTCACCACAACATGAGGCC 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seqdata.uspto.gov/sequence.html?DocID=20020155564
      DB 24;
                                                         69;
   Score 83.6; DB 24
Pred. No. 9.9e-14;
                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABX16390 standard; DNA; 659158
3.5%;
ilarity 67.3%;
Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JAN-2001; 2001US-0771208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse high growth region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Medrano JF, Bradford E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REGC ) UNIV CALIFORNIA
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                                 Local Similarity
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useful for monitoring the efficacy of a drug against depression.
                                           Sequence 10917 BP; 2423 A; 2842 C; 2929 G; 2706 T; 17 other;
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                                                                                                                                                                                                                                                                                                                                                                            CACAACATGAGG 385
                                                                                                              Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYVA-) UNIV VANDERBILT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Organ EL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-526456/48.
                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9739119-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus sp.
                                                                                                                                                                                                                           257
                                                                                                                                                                                                                                                                                                                                                                            374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV06155;
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                                                                            Query Match
Best Local
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                                                                                                                                               439418 rchagachagrachtchaccharggmrichachtchichhagrachtchana 439359
                                                                                                                                                                                                                      439358 fr--creceraceararcaeacarecrecararcaeararrecarrareacaraare 439301
                                                                  . 2
                                                                                                                                                                                                                                                                377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents the genomic DNA sequence of the wild-type mouse Wolfram Syndrome 1 (WFS1) gene used in the method of the invention. The specification describes a non-human transgenic mammal comprising a genome containing a single copy of a wild-type WFS1 gene and a modified WFS1 allele containing a mutation that disrupts the function of WFS1 allele containing a mutation that disrupts the function of wolframin, or its transgenic progeny. Wolframin is a predicted transmembrane protein expressed in many tissues including pancreas and brain. The transgenic nonhuman animals are useful as models for depression, particularly as models for depression in humans. The animals exhibit chronic stress-induced neurochemical and behavioural changes associated with depression. The transgenic animals are also useful for screening or identifying antidepressant agents, drugs or genes that may be employed to ameliorate or treat depression. The animals are also
                                                                                                            198 TCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGGGGGAATCAAACGACCCT 257
                                                                                                                                                                                   258 TTACAGGGGTCACATATCATCTATCCTATATGTCAGGTATTTACATTACGATTCGTAACA 317
Sequence 659158 BP; 177521 A; 147222 C; 149414 G; 184754 T; 247 other;
                                                                                                                                                                                                                                                            GTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATTGAAGGTCACCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            depression, for monitoring the efficacy of a drug against depression, and for screening antidepressants, drugs or genes for ameliorating or
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ne 1; WFS1; transgenic; wolframin; brain; depression; neurochemical change; behavioural change; mouse;
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                                        Length 659158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New transgenic non-human animals (mice), useful as models for
                                                     1.3e-11;
thes 50; Indels
                                        DB 25;
                                                         Pred. No. 1.3e-
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wild-type mouse Wolfram Syndrome 1 gene.
                                      Score 82;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 19; Page 60-63; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВЪ
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                                    Query Match 3.5%;
Best Local Similarity 71.8%;
Matches 135; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                         439241 ACATGTGG 439234
                                                                                                                                                                                                                                                                                                                                  378 ACATGAGG 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wolfram Syndrome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       stress-induced
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10340 TGCGAGGACAGAGGTTCTCAACCTGTGGGGCACAACCCCTTTGGGG--TTTGAATGACTT 10397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention describes nucleic acid sequences isolated from rat. The sequences of the invention comprise 70 viral infection (VI) genes and 8 tumour suppressor (TS) genes. Propagating cell cultures in the absence of the serum protein (SP) allows selective elimination of cells persistently infected with a virus from the cell culture. Inhibitors of the SP can be used for reducing or inhibiting a viral infection. Inhibitors of the TS gene products can be used to suppress a malignant phenotype (MP). The methods and inhibitors can be used with viruses such as HIV, influenza, hepatitis virus or animal retroviruses such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10458 GACAGTAGTAAAATTACAGTTATGCAGTAGCAATGAAAATAATTTTATGGTTGGCGGGTGAC
                                                                                                                                                     197 ITCTAGGGCAGCAGTTCTCAACCTGGGGCCTCGACCCCTTTGGGGGGAATCAAACGACCC
                                                                                                                                                                                                                                                                                                                                                                                            10398 TTCACAGGGGTTGCTTGCCAAAGACCATCAGAAAACACAGGTATTTACATTCCAATTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 AACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGAAGGTCAC
                                                                                                                                                                                                                                                                                                                   TTTACAGGGGTCACATATCA - - - TCTATCCTATATGTCAGGTATTTACATTACGATTCGT
                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genes involved in viral infection and tumour suppression - used to develop products for reducing or preventing viral infection or for suppressing tumours
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Length 10917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viral infection; tumour suppressor; cellular gene; rat; cancer serum protein; inhibitor; malignant phenotype; HIV; influenza; hepatitis; retrovirus; immunodeficiency; ds.
Score 80.4; DB 24; Length
Pred. No. 3.9e-12;
0; Mismatches 51; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viral infection gene SEQ ID NO:75.
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        3.4%;
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119 cacgracaragaragrcaaarcragagcacrgrrrcraraccrgrgagrrgcaacccr 178
                                                                                                                                                                                                                                                                                                              237 TTGGG---GGAATCAAACGACCCT-TTACAGGGGTCACATATCATCTATCTTATGTCA 292
                                                                                                                                                                                                                                                                                                                                                                                              293 GGTATTTACATTACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAAT 352
                                                                                                                                                                                                                                                                                                                                                                                                                          239 AATATTTACATTATGATTCATAGTAGTACCAGAATTACAGTTATGAAGTTACA---AAAT 295
anemia virus, caprine arthritis encephalitis virus or visna virus. Because the identified genes are non-essential to cell survival, the treatment methods can be used in subjects without serious detrimental effects to the subjects.
                                                                                                                                                                                                                                 177 CICITICAGGAICAGCCIGATICIAGGGCAGCAGTICICAACCIGGGGCCICGACCCT
                                                                                                                                                                                           7; Gaps
                                                                                                                                          Query Match 3.3%; Score 78; DB 18; Length 892; Best Local Similarity 70.5%; Pred. No. 5e-12; Matches 148; Conservative 0; Mismatches 55; Indels
                                                                                                         Sequence 892 BP; 224 A; 206 C; 185 G; 229 T; 48 other;
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Search completed: November 14, 2003, 04:10:52 Job time : 613.653 secs

191.6 8.1 478 12 BI293043 BF543101 183 7.8 434 10 BF543101 BF543101 171 7.3 488 9 AN252440 AW252440 171 7.3 511 9 AW351306 AW251306 167.8 7.1 370 9 A7710529 AU139209 131.8 5.6 735 9 AU139209 AU139209 119.6 5.1 509 10 BE627514 BF62751 116.2 4.9 552 28 AQ480395 AQ480473	14 114.6 4.9 518 28 AZ114168 AZ114161 AZI14161 AZII4161 AZIIA161 AZIIA1AZIIAI AZIIAIAI AZIIAIAI AZIIAIAIAI AZIIAIAIAI AZIIAIAIAIA	C 29 103.2 4.4 574 28 AZZ59235 BZZ59245 BZZ59248 GZ5229 BZZ64838 BZZ64838 BZZ64838 BZZ64838 BZZ64838 BZZ64838 BZZ64838 BZZ94836 UT-R-BTI- 31 102.6 4.4 4810 29 BZZ64838 BZZ9485 GZ720-315 33 101.8 4.3 774 28 AZZ4969 AZZ4689 BZZ18693 CZ730-525 C 34 101.6 4.3 594 BZZ778894 AZZ778894 AZZ778894 ZM0014404 C 37 101 4.3 596 28 AZZ56151 AZZ778894 AZZ778894 ZM0014404 C 37 100.8 4.3 600 12 BGG30392 BZZ9595 CZ720-98 42 100.4 4.3 591 28 AZZ4598 BZZ23957 CZ720-298 42 100.4 4.3 803 29 BZZ234545 BZZ34545 CZ720-427 44 100.2 4.2 1085 29 BZZ23957 AZC60257 RPCI-23-4 AZIGNMENTS	RESULT 1 BH043261 LOCUS DNA linear GSS 17-JUL-2001 BH043261 BH043261 BH043261 BH043261 BH043261 ACCESSION WERSION BH043261 BH043261 WERSION SET WERSION GSANISM WAS musculus (house mouse) WERSION BH043261.1 GI:1482512 GSS. SOURCE ORGANISM WAS musculus (house mouse) Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 600) AUTHORS Taegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E., TITLE MOUSE BAC End Sequences from Library RPCI-24 JOURNAL CONDAIL: Shaying Zhao Other GSSs: RPCI-24-330A6.TV CONTACT: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0208 Email: szhao@tigr.org Clones are derived from the mouse BAC library RPCI-24. For BAC
GenCore version 5.1.6  Copyright (c) 1993 - 2003 Compugen Ltd.  OM nucleic - nucleic search, using sw model  Run on: November 14, 2003, 03:46:27 ; Search time 4902.75 Seconds (without alignments)	Title:  US-10-005-337A-1  Perfect score: 2358 Sequence: 1 ggatccttcatgtttaacacaggtcggaggccaccatgg 2358 Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0  Searched: 22781392 seqs, 12152238056 residues  Total number of hits satisfying chosen parameters: 45562784 Minimum DB seq length: 0 Maximum DB seq length: 0	ocessing: Minimu Maximu Maximu Listin: EST:*  2: em_ 2: em_ 4: em_ 7: em_ 11: gb 11: gb 11: gb	10   em_gss_lnv:*   18   em_gss_lnv:*   19   em_gss_lnv:*   19   em_gss_lnv:*   10   em_gss_lnv:*   10   em_gss_lnv:*   20   em_gss_vri:*   21   em_gss_vri:*   22   em_gss_pro:*   23   em_gss_pro:*   24   em_gss_pro:*   25   em_gss_pro:*   26   em_gss_pro:*   27   em_gss_pro:*   28   gb_gss_i**   29   gs_gss_i**   29   gs_gss_i**   29   gs_gss_i**   20   gs_gss_i**   30   gs_gss_i**   31   gs_gss_i**   31   gs_gs_i**   31   gs_gs_i**   32   gs_gs_i**   31   gs_gs_i**   31   gs_gs_i**   32   gs_gs_i**   33   gs_gs_i**   34   gs_gs_i**   35   gs_g

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Moublished by Sequences From Library Reclassification Department of Education Sequences From Library Reclassification Sequences Registry Contact: Shaying Zhoo Genomics Contact: Shaying Zhoo Department of Eukaryotic Genomics Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Email: schaodetigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong Clones are derived from the mouse BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 105 row: P column: 3
Seg primer: SP6
Class: BAC ends.
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/clone lib="RPCI-2"
/clone lib="RPCI-2"
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/note="Torgan: Kidney/Brain; Vector: pBACe3.6; Site_l:
/note="Torgan: Kidney/Brain; Vector: pBACe3.6; Site_l:
/note="Torgan: Page of the pack of the partially digested brain genomic DNA was isolated and partially digested brain genomic DNA was cloned into percent pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DHIOB electrocompetent cells (BRL Life Technologies). "
                                                                                                                                                                                                                                                                                                                    Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, J. Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M. Mouse BAC End Sequences from Library RPCI-23
                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 586)
                                                                        RPCI-23-105P3.TJ RPCI-23 Mus musculus genomic clone RPCI-23-105P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 TGTAAGTGTGATGCACACAGTGCTTGCATTTTCTTGATACGTTAGTCAT-TATTATCTGACA
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98.5%; Pred. No. 8.6e-127;
iive 0; Mismatches 6; I
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Mus musculus
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inbrary availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 330 row: A column: 6
Seg primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
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/note="Vector: pTARBAC1; Site 1: BamH1; Site 2: BamH1;

RPCI-24 Mouse BAC library produced by Pieter de Jong. The library was coloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 TTCTCAACCTGGGGGCCTCGACCCCTTTGGGGGAATCAAACGACCCTTTACAGGGGTCAC
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/strain="C57BL/6J"
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BY091041 RIKEN full-length enriched, 10 days neonate heart Mus
musculus cDNA clone K630084E21 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                            2185 GGGGTGTGACTTGGCTTCCCAGGCTGGAAGATTATCTCACCCAGCCCTAGCTATATAACG 2244
                                                                                                                                                                                                 CCAGACACTAAGTCTGGAATGAAAATTCACCTGCTCTGAATTGGCCACTGGTGGGGGCA 2184
                                                                                                                                                                                                                                                     359 CCAGACACTAAGTCTGGAATGAAATTCACCTGCCTCTGAATTGGCCACTGGTGGGGGGCA 418
                                                                                                                                                                                                                                                                                                                                                               419 GGGGTGTGACTTGGCTTCCCAGGCTGGAAGATTATCTCACCCAGCCCTAGCTATATAACG 478
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             479 GGCTGGTGGGGGGGCCTCCACAGGGCCCAGTTCCAGGGGTTCATCCACATGAGAAAA 537
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299 TCACATTTCTTCCTGATTCGCATACGCCGGGCCAGCTTGTCTCTCCCTCTTGGGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
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BY091041
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Computer Characters Mann. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Flusher details.
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,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakai,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission.
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                                                                                                                                                                      Computational Analysis of Full-Length Mouse cDNAs Compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="heart"
/dev_stage="10 days neonate"
/clone_lib="RIKEN full-length enriched, 10 days neonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2008 TACGTGGGATGACTCGCATTGCTGAGCGGTGTGGTCACTGCCAAAGGAATGACCCTCTCA
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Pred. No. 1.8e-72;
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KEYWORDS SOURCE ORGANISM

VERSION

REFERENCE AUTHORS

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BI293043
UI-R-DKO-cdj-f-07-0-UI.sl UI-R-DKO Rattus norvegicus cDNA clone
UI-R-DKO-cdj-f-07-0-UI 3', mRNA sequence.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Fax: 319 315 9565
Email: bento-soares@uiowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the Not! site and the oligo-dT track served to identify it as a clone from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 478)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                             /dev stage="10 days neonate"
/clone_lib="RIKEN full-length enriched, 10 days neonate
heart"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 CACATITICITICCIGATICGNATACGCCGCGGNCAGCTIGICATCTCCCTCTTGGGCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 CAGACACTAAGTCTGGAATGAAAATTCACCTGCCTCTGAATTGGCCACTGGTGGGGGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2186 GGGTGTGACTTGGCTTCCCAGGCTGGAAGATTATCTCACCCCAGCCCTAGCTATATAAACGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGACACTAAGTCTGGAATGAAAATTCACCTGCCTCTGAATTGGCCACTGGTGGGGGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2006 GATACGTGGGATGACTCGCATTGCTGAGCGGTGTGGTCACTGCCAAAGGAATGACCCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2066 CACATTICTICCTGATTCGCATACGCCGCGGCCAGCTTGTCATCTCCCTTTGGGCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 13; Length 353;
                                                                                                                                                                                                                                                                                                                               2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 11.4%; Score 269.6; DB 13; Length Best Local Similarity 95.5%; Pred. No. 2.8e-62; Matches 298; Conservative 0; Mismatches 11; Indels
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'organism="Mus musculus"
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                                                                                                  /db_xref="taxon:10090"
/clone="K630022E19"
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Rattus norvegicus
                                                                                                                                                                              tissue_type="heart"
                                                                                                                                                                                                                                                                                                                               102 g
                      /mol_type="mRNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                 Nammalia burneria; Rodentia; Sciurognachi; Miridae; Mutinae; Musico, Mikaido, T. Osato, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, T., Osato, M., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomatu, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, T. A., Eretcher, C.F., Forrest, J. E. Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Kanai, H., Kawai, H., Mackana, N., Jackson, I. J., Jarvis, B.D., Kanai, H., Kawai, H., Mackana, N., Jackson, I. J., Jarvis, B.D., Kanai, H., Kawai, H., Mackana, N., Jackson, I. J., Jarvis, B.D., Kanai, J. Kanai, H., Marlais, I., Machais, I., Redi, J., Redi, J., Rayai, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenka, Y., Taylor, M.S., Teasdale, M., Shimada, K., Sultana, R., Maynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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lki.http://genome.gsc.riken.go.jp,

Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Aizawa,K., Akimura,T., Arakawa,T., Tenh,M., Kawai,J., Konno,H., Miyazaki,A.,

T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,

Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,

Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
Submission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Yoshihide Hayashizaki
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1. .353
                                                                        Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 420, 563-573 (2002)
GI:26185447
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BY079997.1
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JOURNAL MEDLINE PUBMED COMMENT

TITLE

source

FEATURES

2185

181

121

7

Gaps

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2245

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/strān="Sprague-Dawley"
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/lab_host="nBH108" [Life Technologies)"
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polylinker; Site_l: Not I; Site_2: Eco RI; The UI-R-AGI
library is a normalized library constructed from 13 dpc
rat ventricle. The tag is a string of 6 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF543101
UI-R-AG1-aal-b-08-0-UI.rl UI-R-AG1 Rattus norvegicus cDNA clone
UI-R-AG1-aal-b-08-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of lowa 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 8250
Email: bento-soaces@uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at LUNL (info@image.llnl.gov). IMAGE ID= 1790595 The following repetitive elements were found in this cDNA sequence: 45-167,
                                                                                                                                                                     ----GTCACATATCATCTATCCTGTATATCAATATTCA 255
                                                                                                                                                                                                                                                                                     241 GGGAATCAAACGACCCTTTACAGGGGTCACATATCATCTATCCTATATGTCAGGTATTTA 300
                                                                                                                                                                                                                                                                                                                                                                      GATTGAAGGTCACCACCACATGAGGCCGCCACACTGTTCTAGAGAAAAATCACCTGGGTG 420
                                                                                                                                                                                                                                                                                                                                                                                                                              194 GGTTGAGGGTCACCACATGAGGCCCACCACACTGTTCTGGGGGAA---CAGTGGAGAG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 GGGAAAGGTTTGGGAAAGCCTTTCTGTCCATTCTTCAAAGTGAAGTGTTCACA 480
         TTCAGGATCAGCCTGATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137 AGGAAAGGATTGAGGAAGCC-TTCCATCTGTTCTGCACTCTTCAAAGGGATGTATTCACA 79
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                               CATTACGATTCGTAACAGTAGCAAATTACAGGTATGAAATAGCAATGAAATTTTTAT
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                                                                    TTCAGGGTCAGCCTGATTCTAGGGCAGCAGTTCTCAACCTGGA-
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Rattus norvegicus
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Location/Qualifiers
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//dev stage="Thing (Life Technologies)"
//clonellb="UUI-R-DKO"
|/dev stage="Thing (Life Technologies)"
//clonellb="Uui-R-DKO"
|/dev stage="AbDUT"
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normalized rat heart pool library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 170-292, vURRLA#DNA/MER! type Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCTTTGCCACCCATGAATACTTCCTAGTCTAGTCCGTTTGTGAAACTCAGCCCATCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   417 GCTINIGCCACCCAIGAACACATCCIAGICCCTCCCCTITGTGAAATICAGCCCATTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ACACTICIGCAAGCCCCAICCICIACAAGGIGCICATIGGGAAITICCIGGAGCTICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----GGTTCTGTCCCGAAGCTTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGÁTCCTCTAATGTTTAACAAATGACAAGCTAGCCCA--GGGGAAAGACTGCCTGACAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,4e-41;
nas 80; Indels
                                                                                                                                                                                                                                                                                           /mol_type="mRRA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-DK0-cdj-f-07-0-UI"
                                                                                                                                                                                                                                            1. .478
/organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 8.1%; Score 191.6; Best Local Similarity 69.5%; Pred. No. 7.4 Matches 372; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=rat heart pool
                                                                                                                                                                                                                Location/Qualifiers
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103 c 110 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357 ACA
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ORIGIN
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/dev stage="adult"
//lab_host="adult"
//lab_host="adult"
//lab_host="DH10B (Life Technologies)"
//clone_lib="uu-R-B10"
//note="Vector; pT713-Pec (Pharmacia) with a modified
//note="Vector; pT713-Pec (Pharmacia) with a undified
//note="Vector; pT713-Pec (Pharmacia) with a ur-R-BJ0
library is a subtracted library derived from the UI-R-BJ0
UI-R-AB1, UI-R-AC1, UI-R-AD1, UI-R-AB1, UI-R-AB1, and
UI-R-AG1 libraries. These libraries represent tissues from
rat atrium at 16.5 dpc, ventricle at 16.5 dpc, AV canal
at 16.5 dpc, atrium at 15 dpc, ventricle at 13 dpc. AV
canal at 15 dpc, and ventricle at 13 dpc. The tag is a
string of 5-6 nucleotides present between the Not I site
and the oligo-dT track. The library was constructed as
described by Bonaldo, Lennon and Soares, Genome Research
6: 791-806, 1996.
normalized AV canal at 15 dpc library cDNA Library Preparation:
M.B. Scares Lab Clone distribution: clones will be available
through Research Genetics (www.resgen.com) The following repetitive
elements were found in this cDNA sequence: 1-44,
PoLY A#Simple repeat
Seq primer: M13 Forward
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UI-R-BJO-adg-f-04-0-UI.sl UI-R-BJO Rattus norvegicus cDNA clone
UI-R-BJO-adg-f-04-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  289 ----CACTAGGAGAGAGAGAACCCACGAAGGA-----TATCAGTGTGCTGGTTTTCCAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 AATGTCTCATTCCGAAGGTTCTAGAAACACAGTTTACTGGATGAAGAGCTGAAGTGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      349 ATGGAAACCAGAAGCCCAACAGTTGTCCTTCGATAGTGTCTCTGAGACAGCCCAGGACAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 GCCAGCAT----ACAAACATAACATTAATGCTTCCCTCTGCTACTGACACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      879 ATGAAAACGAGAAGACCAACAGTTATCCATTGATAGCGTCTCAGGACAGATAGGACAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       939 AGAACACTAGGAGAGGGGAACCCACGAAGGACAAGGTATTAGTGTGTTGGTTTTCAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         999 AATGICITGIACIGAAGAIICIAGAAACACAAAIIIGCIGGIIGAACAGCIGAAGIGGGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55; Indels
                                                                                                                                                                                                                                                             /mol_type="mRNA"
/strain="Spraque-Dawley"
/strain="Spraque-Dawley"
/clone="Ul-R-BJO-adx-e-05-0-Ul"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1176 CTTCACTCTCTCTTCATAAAAAAAAAAA 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 171; DB 9;
Pred. No. 3.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6:791-806, 1996.
TAG_LIB=UI-R-BJO
TAG_TISSUE=AV canal at 15 dpc
TAG_SEQ=GAAGG"
a _111 c 106 g 155 t
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                                                                                                                                                                                                                  1. .488
/organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                           Location/Qualifiers
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Best Local (
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AW251306/c
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UI-R-BJO-adx-e-05-0-UI.sl UI-R-BJO Rattus norvegicus cDNA clone
UI-R-BJO-adx-e-05-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                   261 CAGGGGTCACATATCATCTATCTATATGTCAGGTATTTACATTACGATTCGTAACAGTA 320
                                                                                                                                                                                                                                                                                                                                             43 CTGGAGTCACATATCATCTGTATATCAAATATTCACATCATGACTCATAACAGTA 102
                                                                                                                                                                                                                                                                                                                                                                                                                    GCTGGGGCTCTTAGTAAGTCTGAGTAGGAACTGTATGTACCAGGTCTGCTTCTTATGGGT 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  561 GGAGCCAAGACGCATCGTGGGTGGAGCGAAGACGCAACCTCCACCTTCTAGCTCTGCATCC 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 ACACAATTACAGGCATGATGTAGCAATGAAATGATTTTATGGTTGAGGGTCACCACCACA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTTGGGGCTCTTAGTAAATCTGAGCAGAACTGCACCAGGAAATTTT--ATCTGGTTTTG 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                337 TGATTTTCTGCTTCTCCTGNGTGGAACCAAGACTGGACTCCATTGTCTAGCCCTGCATCT 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: benco-soarces@uiowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
            present between the Not I site and the oligo-dT track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996. Tissue provided by Jim Lin, Department of Biology, University of Iowa." 17 there
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 -TTCCATCTGTTCTGCACTCTTCAAAGGGATGTATTCACAGAAAGCCTTTGGTCGGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 TGAGGCCACCACACTGTTCTGGGGGAA---CAGTGGAGAGGAGGAAAGGATTGAGGAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITCIGICCATICITCATICITCAAAGIGAIGIGITCACAGAAAGCCITITCAGCIGITCI
                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                  Length 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Iowa 375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, TE1: 319 335 8250 Fax: 319 335 9865
                                                                                                                                                                                                                                                                  96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                  Score 183; DB 10;
Pred. No. 1.6e-38;
                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Res. 6 (9), 791-806 (1996)
97044477
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AW252440.1 GI:6596031
                                                                                                                                                                                                               Query Match 7.8%;
Best Local Similarity 73.0%;
Matches 276; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   621 ATAGCAAGTAGCCTAATG
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TITLE
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University of Iowa 1750 Computations Scholls School Diversity of Iowa 1750 Newton Road , 4156 MEBRE, Iowa City, IA 52242, USA Tel: 319 315 9256
Fax: 319 315 9266
Fax: 310 315
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/mol_types="Rattus norvegicus"
/atrain="Sprague-Dawley"
/dev_stref="Laxon:10116"
/clone="UI-R-AG1-aal-b-08-0-UI"
/dev_stage="adult"
/dev_stage="adult"
/clone="UI-R-AG1-aal-b-08-0-UI"
/clone="UI-R-AG1"
/clone="UI-R-A
                                                                                                                                                        EST 04-JUN-1999
         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 370) Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
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UI-R-AG1-aal-b-08-0-UI.sl UI-R-AG1 Rattus norvegicus cDNA clone
UI-R-AG1-aal-b-08-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                        GCCAGCAT----ACAAACATAACACCCTAATTAATGCTTCCCTCTGCTACTGACACTCT
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                                                                                                                                                                                                                                                                                                                                                    TAG LIB=UÎ-R-AG1
TAG<sup>T</sup>ISSUE=ventricle at 13 dpc
TAG<sup>S</sup>EQ=CAGGGA"
                                                                                                                                                                                                                                                                                                                                                                                                          CCCTTCATCTTCATAAAATAAACAAACA 13
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TITLE
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/ bitalin="spirals">
/ bitalin="spirals">
/ bitalin="spirals">
/ bitalin="spirals">
/ dev_Estage="adult"|
/ dev_Estage="adult"|
/ lab_host="bit00" (life Technologies)" |
/ clone lib="UI-R-BJO" |
/ clone lib="Will-R-BJO" |
/ clone lib="Will-R-BJO" |
/ clone lib="Will-R-BJO" |
/ lone lib="Will-R-BJO" |
/ lone lib="Will-R-BJO" |
/ lone lib="Will-R-BJO" |
/ library is a subtracted library/derived from the UI-R-BJO |
/ UI-R-BJI, UI-R-ABI, UI-R-BJO |
/ UI-R-BJI ilbraries These libraries represent tissues from rat atrium at 16.5 dpc, ventricle at 16.5 dpc, AV canal at 15.5 dpc, atrium at 15 dpc, ventricle at 16.5 dpc, AV canal at 15.5 dpc, and ventricle at 13 dpc. The tag is a string of 5-6 nucleotides present between the Not I site and the oligo-dT track. The library was constructed as as and the oligo-dT track. The library was constructed as as a constructed a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1058
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                                                                                                                                                                                      1 (bases 1 to 511)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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Best Local Similarity 78.4%; Pred. No. 3.3e-35;
Matches 261; Conservative 0; Mismatches 55; Indels 17; Gaps
                                                      Craniata, Vertebrata, Euteleost.
Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University of Iowa
315 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
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TAG_LIB=UI-R-BJO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
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/organia="Rattus norvegicus"
/mol type="mtNA"
/strain="Sprague-Dawley"
                                                                                                                                                                                                                                                                                                                                                              Genome Res. 6 (9), 791-806 (1996) 97044477
Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: bento-soares@uiowa.edu
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_120 c 113
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                                                                                                                                                                                                                                                                                                                                     discovery
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ORGANISM
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TITLE
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COMMENT
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/tissue_type="Thymus"
/dev_stage="4 weeks"
/dev_bote="MuloB"
/dlone_lib="Soares thymus_2NbMT"
/clone_lib="Soares thymus_2NbMT"
/clone_lib="Soares thymus_2NbMT"
/clone_Type="Thymosoares thymus_2NbMT"
/clone_Type="Thymosoares thymus_2NbMT"
/clone_Type="Thymosoares"
/clone_Type="T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BB627514 50ares_thymus_2NbMT Mus musculus cDNA clone
IMAGE:3375590 5' similar to gb:L35933 Mouse erythrocyte protein 4.2
                                                                                                                                                                                                                            2224
                                                                                                                                                                                                                                                                                                                                                                                            148 ccesciccascitatatasacitascicaterasasas 207
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                            2165 ATTGGCCACTGGTGGGGGCAGGGGTGTGACTTGGCTTCCCAGGCTGGAAGATTATCTCAC
                                                                                                                                                                                                                                                                                                                                        CCAGCCCTAGCTATATAA - CGGGCTGTGTGGAGGGGCTCCACAGGGCCCAGTTCCAGGGG
                                                                                                                                                            28 TCCCTCCCTTCACTTCCCAGACACTGAGTCTGGAATGAAATTCACCTGCCTCTGA
                                                                                                                                                                                                                                                                                    88 griggerecraargggggggggggggrgrracricggricccaggriggaagarrarcreac
                                                                                                                    2105 TCATCTCCCTCTTGGGCTTCCCAGACACTAAGTCTGGAATGAAAATTCACCTGCCTCTGA
                                                             Gaps
                                                       .,
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Pred. No. 4e-21;
Length 735;
     DB 9;
  Score 131.8; DB 9
Pred. No. 2.1e-24;
0; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 rrccrrc-caccacacacacaraca 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
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/organism="Mus musculus"
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/clone="IMAGE:3375590"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2284 TTCATCCACAGAGAGAAAAACATAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seg primer: -40RP from Gibco
High quality sequence stop: 4
Location/Qualifiers
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/strain="C57BL/6J"
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Mus musculus
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                                                             Conservative
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                               Similarity
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        Query Match
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                                                                                                                                                                                                                                                            348 ATGGAAACCAGAAGGCCAACAGTTGTCCTTCGATAGTGTCTCAGGACAGCCAGGACAGAG 289
                                                                                                                                                                                                                                                                                                                                                    ----CACTAGGAGAGAGAGAAGCCACGAAGGA-----TATCAGTGTGCTGCTGCTAGGGGC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237 AATGICTCATICCGAAGGIICIAGAAACACAGTITACIGGAIGAAGAGCCIGAAGIGGGGI 178
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 735)
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HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Nesearch Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                    939 AGAACACTAGGAGAGGGGAACCCACGAAGGACAAGGTATTAGTGTGTTTTTCAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 GCCAGCAT----ACAAACATAACACCCTAATTAATGCTTCCCTCTGCTACTGACACTCT
                                                                                                                                              Gaps
                                                                                                                                              17;
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AU139209 PLACE1 Homo sapiens cDNA clone PLACE1010155
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
17El: 81-438-55-3975
Fax: 81-438-52-3986
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Pred. No. 2.2e-34;
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db_xref="taxon:9606"

/clone="plaCE1010155"

/tissue_type="placenta"

/clone_lib="placenta"

/olone="Vector: pME18SF13"
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human cDNA project
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Genomics Laboratory
                                                                                    Query Match
Best Local Similarity 77.8%;
Matches 259; Conservative
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electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors a purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQ480395 11-236B22.TV RPCI-11 Homo Rapiens genomic clone RPCI-11-236B22
                                                                                                                                                                                                                                                                                                                                                                                                                                       390 TTCTAAGGCAATCTCTCTCAACCTACGGGTTTCGACCCCTTTGGG-----TATCAACCCT 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            335 TICACAGGGGTCACATATCACATATTCTGCATGTCAGATATTTACAGTTCATAAC 276
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Clones are derived from the human BAC library RPCI-11. For BAC

Library availability, please contact Pieter de Jong

(pieter@dejong, med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genet cs (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 522)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
                                                                                                                                                                                                                                                                                                                                                                                       197 TTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGGGGGAATCAAACGACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257 ITTACAGGGGTCACATATCATCTATCTATATGTCAGGTATTTACATTACGATTCGTAAC
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                                                                                                                                                                                                                                                                                   Length 538;
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Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                Score 116.2; DB 28; Length
Pred. No. 3.5e-20;
0; Mismatches 33; Indels
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/db_xref="GDB:7590285"
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/clone="RPCI-11-236B22"
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Best Local Similarity 79.99
Matches 151; Conservative
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215 AACATGAGG 207
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                                                                               374
                                                                                                                                                                                                                                                        GTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATTGAAGGTC 371
                                                       CCTGATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTTGGGGGGATCAAAC 251
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ804735 S38 bp DNA linear GSS 20-FEB-200
2M0065113R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0065113 R, genomic survey sequence.
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus CS7BL/61 (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                    252 GACCCTTTACAGGGTCACATATCATCTATCCTATATGTCAGGTATTTACATTACGATTC
                                                                                                                                                                                    432 TACT-TTCACAGGGGTAGGCTATCAGGTATCCTGCATATCAGATATTACATTATGATTC
     Gaps
     1;
     Indels
     39;
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Insert Length: 10000 Std Error: 0.00
Plate: 0065 row: I column: 13
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
  0; Mismatches
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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University of Utah Genome Center
University of Utah
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/clone="UUGC2M0065113"
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Mus musculus
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  Conservative
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Fax: 801 585 7177
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84112, USA
  154;
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Location/Qualifiers
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             clone lib="RPCI-23"
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Best Local Similarity 67.2%;
Matches 162; Conservative (
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AZ290439/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgan.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 49 row: H column: 23
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 518)
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                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Male"
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
RPCIII Human Male BAC Library"
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Contact: Shaying Zhao
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
                                                                                                                                                                                                                                     1540 TCTCTCTGTGCATCACTTCGGCCCGTTTTGGGGT--AGATCCTCTGATTAGCCTTCAGAT
                                                                                                                                                                                                                                                                                                                                               142 TTAGAACACGGTAAGCATGTCATGTGCTAATTATGGCCAGTGACATCATAAAAGAAAAGT
                                                                                                                                                                                                 Gaps
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                                                                                                                                                       Query Match 4.9%; Score 116; DB 28; Length 522; Best Local Similarity 76.7%; Pred. No. 3.9e-20; Matches 155; Conservative 0; Mismatches 45; Indels
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/lab_host="DH10B"
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Mus musculus
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/note=Torgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
BCORI; Site_2: BCORI; Female C57BL/6J mouse kidney and/or
Brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
Belected DNA was cloned into the pBACe3.6 vector at the
BCORI sites. The ligation products were transformed into
DHIOB electrocompetent cells (BRL Life Technologies). "
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Clones are derived from the mouse BAC library RPCI-23. For BAÇ

Clones are derived from the mouse BAC library and albituary and albituary and albituary and albituary and long library and long from end. buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Plate: 59 row: G column: 22
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 596)
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Pred. No. 9.4e-20;
0; Mismatches 79; Indels 0;
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Other GSSs: RPCI-23-59G22.TJB
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
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/sex="Female"
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brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
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Best Local Similarity 78.33
Matches 148; Conservative
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Sequence 75, Application US/09171209

Sequence 75, Application US/09171209

GENERAL INFORMATION:

APPLICANT: VANDERBILT UNIVERSITY

305 Kirkland Hall

Nashville, TN 37240

TITLE OF INVENTION: MAMMALIAN GENES INVOLVED IN VIRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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69.2%; Pred. No. 3.9e-16;
tive 0; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17, Application US/08920422A
Fatent No. 6255473
GENERAL INFORMATION:
APPLICANT: Witek, Michael P.
APPLICANT: Mitsuda, No. 6255473iaki
APPLICANT: Roses, Allen D.
TITLE OF INVENTION: Presentilin-1 Gene Promoter;
FILE REPERENCE: VITEKPRESENLIN
CURRENT APPLICATION NUMBER: US/08/920,422A
CURRENT PILING DATE: 1997-08-29
NUMBER: OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
4 US-09-578-178-3

4 US-09-577-806-3

1 US-09-007-005-14

3 US-09-007-005-3

3 US-09-244-796-3

5 4 US-08-646-2508-1

5 PCT-US95-05616-1

5 PCT-US95-05616-1

3 US-08-846-705-4

3 US-09-220-132-168

4 US-08-846-704-3

3 US-09-078-294-4

3 US-09-078-294-3

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4 US-08-661-018A-1

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ORGANISM: Mus musculus
US-08-920-422-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 135; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-920-422-17/c
      SEQ ID NO 17
LENGTH: 48
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      RESULT
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Sequence 183, Appl
Sequence 183, App
Sequence 183, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 38, Appl
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Appli
                                                                                                                                         November 14, 2003, 03:50:07 ; Search time 134.074 Seconds (without alignments) 7762.738 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 183, 1 Sequence 183, 1
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Sequence 4
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'GqD2_6/ptodata/2/ina/5A_COMB.seq:*
'GqD2_6/ptodata/2/ina/5B_COMB.seq:*
'GqD2_6/ptodata/2/ina/6A_COMB.seq:*
'GqD2_6/ptodata/2/ina/6B_COMB.seq:*
'GqD2_6/ptodata/2/ina/PCTUS_COMB.seq:*
'GqD2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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Compugen Ltd.
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US-09-328-475C-157
US-08-604-333-3
US-09-110-618-3
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US-09-171-209-75
US-09-131-209-75
US-09-218-207-183
US-08-135-511-35
US-08-182-1640-38
US-08-781-891-208
US-08-781-891-208
US-09-781-891-208
US-09-618-166-207
US-08-895-618-107
US-08-895-810D-4
US-08-895-810D-4
US-08-895-810D-4
US-08-131-932-107
US-09-116-186-107
US-09-116-186-107
US-09-113-932-107
US-08-131-932-107
US-08-131-932-107
US-08-131-932-107
US-08-131-932-107
US-08-131-93-107
US-08-131-93-5
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                                                                                                                                                                                                                                                                                                                                                                             569978 segs, 220691566 residues
                     GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                        sw model
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Gapop 10.0 , Gapext 1.0
                                                                                                      - nucleic search, using
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length: 2000000000
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Perfect score:
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Minimum DB e Maximum DB e

Database

Result No.

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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 TTGGG---GGAATCAAACGACCCT-TTACAGGGGTCACATATCATCTATCTTATGTCA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 TTGGGAGTGCGGTCAAATGACCCTATCACAGGGGTCTCAAATGAGATATCCTGCATATCA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293 GGTATTTACATTACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAAT 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 AATATTTACATTATGATTCATAGTAGTACCAGAATTACAGTTATGAAGTTACA---AAAT 295
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                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                  ADDRESSEE: Needle & Rosenberg, P.C.
STREET: 127 Peachtree Street, Suite 1200
                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/171,209
FILING DATE: 08-Mar-1999
FILING DATE: 08-Mar-1999
CLASSIFICATION STANDARD
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/06067
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Selby, Elizabeth
REGISTRATION NUMBER: 38,298
REFERENCE/DOCKET NUMBER: 22000.0061/P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.9e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
3.3%; Score 78; DB
Best Local Similarity 70.5%; Pred. No. 6.9e
Matches 148; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 AATTTTATAGCTGAGAGTCACCACAACATG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cohen, Daniel
APPLICANT: Chen, Daniel
APPLICANT: Blumenfeld, Maxta
APPLICANT: Blumenfeld, Maxta
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: PROSTATE CANCER GENE
FILE REFERENCE: GENEET: 18CPICP
CURRENT APPLICATION NUMBER: US/09/338,907
CURRENT FILING DATE: 1999-06-23
EARLIER APPLICATION NUMBER: 08/996,306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 75:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 183, Application US/09338907
Patent No. 6265546
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 404 688 0770
INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENCE CHARACTERISTICS:
LENGTH: 892 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 404 688 9880 INFORMATION FOR SEQ ID NO: 75:
              NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: Needle
                                                                                                            CITY: Atlanta
STATE: Georgia
                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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Pred. No. 6.5e-12;
0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 183, Application US/09218207
; Patent No. 6346381
; GREERAL INFORMATION
; APPLICANT: Cohen, Daniel
; APPLICANT: Cohen, Daniel
; APPLICANT: Hya, Chumakov
; APPLICANT: Bougueleret, Lydie
; TILLE OF INVENTION: Prostate cancer gene
; FILE REFERENCE: GENSET.018CP1
; CURRENT APPLICATION NUMBER: US/09/218, 207
; CURRENT PILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 08/996, 306
; EARLIER PILING DATE: 1998-12-22
; EARLIER PILING DATE: 1998-12-22
; EARLIER PILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
EARLIER APPLICATION NUMBER: 60/099,658
EARLIER FILING DATE: 1998-09-09
EARLIER APPLICATION NUMBER: 09/218,207
EARLIER FILING DATE: 1998-12-22
SOFTWARE: PALENT. DNOS: 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.2%;
Best Local Similarity 80.0%;
Matches 88; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: exon
; LOCATION: 25520..26016
; OTHER INFORMATION: exon8
US-09-338-907-183
                                                                                                                                                                                                                                                                                LOCATION: 5259..5328
OTHER INFORMATION: exon2
                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: exon
LOCATION: 12675..12791
OTHER INFORMATION: exon3
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OTHER INFORMATION: exon5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION: exon6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION: exon7
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                                                                                                                                                                                                             ORGANISM: Mus musculus
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LOCATION: 21789.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: exon
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LOCATION: 2338
                                                                                                                                        SEQ ID NO 183
LENGTH: 37950
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7215 GAATCTAAGTCAGTGCTTCTCAACCTGTGGATCACAACCCATGTAGGGGGTAGAGTCAAA 7156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 CGACCCTTTACAGGGGTCACATATCATCTATCCTATATGTCAGGTATTTACATTACGATT 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 35, Application US/08187453
Patent No. 5753431
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Cholesterol 7a-Hydroxylase Gene
TITLE OF INVENTION: Regulatory Elements and Transcription Factors
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                 Length 10614;
                                                                                                                                                                                                                                                                                                                                                                                                                                        195 GATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCCTCGACCCCTTTGGGG-
                                                                                                                                                                                                                                                                                                                                                                                           69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/187,453
FILING DATE: 28-JAN-1994
CLASSIFICATION THE: US/08/187,453
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/135,488
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/135,511
FILING DATE: 3-OCT-1993
PRIOR APPLICATION NUMBER: US 08/135,510
FILING DATE: 3-OCT-1993
APPLICATION NUMBER: US 08/135,510
FILING DATE: 13-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 Score 74.6; DB 1;
Pred. No. 3.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                            18748/175
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REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 18748/188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7035 TCACÁCAÁCÁTCAGGAAGGTAGA 7013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                       TELEX: 904136

INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 10614 base pairs
TYPE: nucleic acid
STRANDEDMESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-135-511-35
                            REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
         REGISTRATION NUMBER: 31,298
                                                                                                                                                                                                                                                                                                                                            3.2%;
ilarity 64.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 3000 K Street, CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20007-5109
COMPUTER READABLE FORM:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       276 ATCTATCCTATATGTCAGGTATTTACATTACGATTCGTAACAGTAGCAAAATTACAGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cholesterol 7a-Hydroxylase Gene
Regulatory Elements and Methods for Using Them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9630 cécaararcaacaaararriraregricaeercaceraacereaee 9679
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/135,511
FILING DATE: 13-0CT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, Colin G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 74.8; DB 4;
Pred. No. 6.5e-12;
0; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3000 K Street, N.W., Suite 500 CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 35, Application US/08135511
Patent No. 555899
GENERAL INFORMATION:
TITLE OF INVENTION: Cholesterol 7a-
TITLE OF INVENTION: Regulatory Eler
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 80.00
مال المرابع 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: exon
LOCATION: 25520..26016
CTHOR INFORMATION: exon8
US-09-218-207-183
                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: exonS
FEATURE:
NAME/KEY: exon
                                                                                                                                                                                                                            LOCATION: 12675..12791
OTHER INFORMATION: exon3
                                                                                                                                                             OTHER INFORMATION: exon2
                                                                                                                                                                                                                                                                                                                   LOCATION: 14621..14710
OTHER INFORMATION: exon4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: exon6
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                                                 TYPE: DNA ORGANISM: Mus musculus
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                                                                                                                NAME/KEY: exon
LOCATION: 5259.
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US-08-135-511-35/c
                                                                                                                                                                                                       NAME/KEY: exon
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LOCATION: 23387
                                                                                                                                                                                                                                                                                                  NAME/KEY: exon
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SEQ ID NO 183
LENGTH: 37950
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1312 Griciocia agado - arcricia rario caratrira carca aga a carado de cara de 1369
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                                                                                                                                                                                                                                 206 AGCAGTICTCAACCTGGGGGCCTCGACCCTTTGGGGGAATCAAACGACCTTTACAGGG 265
                                                                                                                                                                                                                                                                                                                                                                                                                                     326 ATTACAGGTATGAAATAGCAATGAA-ATAATTTTATGATTGAAGGTCACCACAACATGAG 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 TAAAAGTCGTAGCAGTGGCAAGATTACGGTTACAAAGTAGCAACGAAAATAATTTTATGC 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
US-09-272-496-7
Sequence 7, Application US/09272496
Fatent No. 6245966
GENERAL INFORMATION:
APPLICANT: DeGregori, James
TILE REFERENCE: 90-98
CURRENT APPLICATION: Adenoviral mediated gene transfer into lymphocytes
CURRENT FILING PET: 199-98
CURRENT FILING PET: 199-03-19
EARLIER APPLICATION NUMBER: US 60/092782
MUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                    266 GICACATATCATCIATCCTATATGTCAGGTATTTACATTACGATTCGTAACAGTAGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195 GATTCTAGGGCAGCAGTTCTCAACCTGGGGCCTCGACCCCTTTGGGGGAATCAAACGAC
                                                                                                                                                                                                                                                                                1252 AGAGCTTTTCAACCTGTGGGTCGTGACCCCTTCACGGAGCCAAACAACCATTCAGAAGG
                                                                                                                                                                               3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 4072;
                                                                                                                                Length 4164;
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                                                                                                                                                                               51; Indels
                                                                                                                           Score 73.4; DB 4;
Pred. No. 4.7e-12;
0; Mismatches 51;
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2.9%; Score 68.6; DB 3;
Best Local Similarity 69.5%; Pred. No. 1.4e-10;
Matches 141; Conservative 0; Mismatches 49;
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US-08-701-891-208/c
Sequence 208, Application US/08781891
Patent No. 6090620
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
                                                                                                                                3.1%;
                                                                                                                             Query Match
Best Local Similarity 70.2
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Mus musculus
US-09-272-496-7
                                                       linear
                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1430 G 1430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         385 G 385
                                                       ; TOPOLOGY:
US-08-882-164D-38
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                  Query Match
3.2%; Score 74.6; DB 1; Length 10614;
Best Local Similarity 64.0%; Pred. No. 3.5e-12;
Matches 130; Conservative 0; Mismatches 69; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-882-164D-38

Sequence 38, Application US/08882164D

Patent No. 6306624

GENERAL INFORMATION:
APPLICANT: Petkovich, P. Martin, White, Jay A.,
APPLICANT: Beckett, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRESCUE Blake, Cassels & Graydon STREET: Box 25, Commerce Court West CITY: Toronto CITY: Toronto COUNTRY: Canada ZIP: MSL 1A9

ZIP: MSL 1A9

COMPUTER READABLE PORM: MSDLUM TYPE: Diskette, 3 1/2 inch, 1.4 COMPUTER: COMPAQ, IBM PC COMPATION SYSTEM: MS-DOS 5.1 COMPUTER: COMPAQ, IBM PC COMPATION SYSTEM: MS-DOS 5.1 CONFERTING NUMBER: US/08/82,164D FILING DATE: Union 21, 1996 APPLICATION NUMBER: 08/67,546 FILING DATE: OCTOBER 1, 1996 ATPLICATION NUMBER: 08/724,466 FILING DATE: OCTOBER 1, 1996 ATPLICATION NUMBER: 1, 1996 ATPLICATION NUMBER: 1, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 862.47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7035 TCACACACATCAGGAAGGTAGA 7013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             371 CACCACACATGAGGCCGCCACA 393
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TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 4164 PARCEL
                                                                      TELEX: 904136
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 10614 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-187-453-35
                            TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Hunt, John C. REGISTRATION NUMBER:
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6043 IGATIGATCAAATGGCTCTTICACAGGGTTTACAAATCAAACATCCTGTATATCAGATAG 5984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 TGGGGGAATCAAACGACCCTTTACAGGGGTCACATATCATCTATCCTATATGTCAGGTAT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 TTACATTACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.9%; Score 68; DB 4; Length 16442;
66.2%; Pred. No. 5e-10;
tive 0; Mismatches 50; Indels
                                                                                               COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/618,166
FILING DATE: 17-Jul-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 207, Application US/08781891

Patent No. 6090620

GENERAL INFORMATION:

APPLICANT: Yu, Chang-En

APPLICANT: Oshima, Junko

APPLICANT: Mulligan, John T.

APPLICANT: Schellenberg, Gerald D.

TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO

TITLE OF INVENTION: WERNER'S SYNDROME
                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: MCMASTELLION:
NAME: MCMASTERS, David D.
RECISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 240052.419C1
TELEPHONNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-631
INFORMATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERISTICS:
LENGTH: 16442 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
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APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
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US-09-618-166-208
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
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Matches 98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and I
STREET: 6300 Columbia
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STATE: Washingtor
COUNTRY: USA
ZIP: 98104-7092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298 TTACATTACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTT 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
                                               APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                           6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5923 rcarggrrggrgccarcacagcagg 5896
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TITLE OF INVENTION: GENE AND GENE PRO
WERNER'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 208, Application US/09618166; Patent No. 6583112; GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
SPLICANT: Fu, Chang-En
Oshima, Junko
Mulligan, John T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERISTICS:
LENGTH: 16442 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                      SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 209
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STATE: Washington
  Yu, Chang-En
Oshima, Junko
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Best Local Similarity 66.2;
Matches 98; Conservative
                                                                                                                                                                                                                              STREET: 6300 Columb
CITY: Seattle
STATE: Washington
COUNTRY: USA
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                                                                                                                                                                                                   ADDRESSEE:
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US-08-781-891-208
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262 AGGGGTCACATATCATCTATGTCTATATGTCAGGTATTTACATTACGATTCGTAACAGTAG 321
                                                   Gaps
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         Length 29604;
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..2618, 2890..3164, 4291..4509, 4598..4709, 4795
..4903, 5017..5117, 5200..5255, 5447..5525, 5598
                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: MINATO, Nagahiro
APPLICANT: HITORI, Masakazu
APPLICANT: HIROSHI, Kubota
APPLICANT: MASATSUGU, Maeda
APPLICANT: MASATSUGU, Maeda
TITLE OF INVENTION: SPA-1 PROTEIN AND GENE CODING THEREFOR
                                                                                                                                                                                                               2.8%; Score 65; DB 2; Length 6645;
                                                                                                                                                                                  322 CAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATTG 365
    Score 65.6; DB 4; Length 2
Pred. No. 4e-09;
0; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/380,403A FILING DATE: 30-JAN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/128/AAOK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION: 133
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/325,909
FILING DATE: 19-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 6-279712
FILING DATE: 20-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 6-139513
FILING DATE: 30-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: WEGISTRATION
REGISTRATION NUMBER: 25,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                               RESULT 13
US-08-380-4013A-4/C
; Sequence 4, Application US/08380403A
; Patent No. 5831024
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3: DNA (genomic)
         2.8%;
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Query Match
Best Local Similarity 76.99
Matches 80, Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COCATION:
LOCATION:
LOCATION:
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LOCATION:
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Pred. No. 4e-09;
0; Mismatches 24; Indels 0;
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Mulligan, John T.
Schellenberg, Gerald D.
STALLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
WERNER'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 322 CAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATTG 365
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ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/618,166 FILING DATE: 1.7-Jul-2000 CLASSIFICATION: CLIOR CLASSIFICATION: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFRENCE/DOCKET NUMBER: 240052.419C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
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                        NAME: NO. 6090620tenburg Ph.D., Carol REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900
INFORMATION FOR SEQ ID NO: 207: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 207, Application US/09618166
Patent No. 6583112
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
Yu, Chang-En
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 29604 base pairs
TYPE: nucleic acid
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Best Local Similarity 76.9%;
Matches 80; Conservative C
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                                                                                                                                                                                                      LENGTH: 29604 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                               US-08-781-891-207
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233 CCCTTTGGGGGAATCAAACGACCCTTTACAGGGGTCACAT--ATCATCTATCTATATGT 290
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                                                                                                                                                           Gaps
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HATTORI, Masakazu
HIROSHI, Kubota
MASATSUGU, Maeda
TITLE OF INVENITON: SPA-1 PROTEIN AND GENE CODING THEREFOR
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
..4903, 5017..5117, 5200..5255, 5447..5525, 5598
..5741)
                                                                                                                 Length 6645;
                                                                                                                                                           40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                      351 ATAATTTTATGATTGAAGGTCACCACACATGAGG 385
                                                                                                                                                                                                                                                                                                                                                                                                                434 AATAATTTTGA-TCAGGGTCACCACACCATGTGG 401
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                                                                                                            2.8%; Score 65; DB 2;
72.3%; Pred. No. 2.5e-09;
tive 0; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 30-JAN-1995
APPLICATION NUMBER: US 08/325,909
FILING DATE: 19-OCT-1994
APPLICATION NUMBER: JF 6-279712
FILING DATE: 20-OCT-1994
APPLICATION NUMBER: JF 6-139513
FILING DATE: 30-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/895,810D
FILING DATE: 17-U1-1997
CLASTICATION: <URNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/380,403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-895-810D-4/c
; Sequence 4, Application US/08895810D
; Patent No. 6406886
; GENERAL INFORMATION:
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(202)672-5399
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SEQUENCE CHARACTERISTICS:
LENGTH: 6645 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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STRANDEDNESS: double
                                                                                                       2.85
Best Local Similarity 72.35
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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                  ; LOCATION:
; LOCATION:
US-08-895-628-4
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                                                                                    CCCTTTGGGGGAATCAAACGACCCTTTACAGGGGTCACAT--ATCATCTATCTATATGT 290
                                                                                                                                                                         291 CAGGTATTTACATTACGATTCGTAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAA 350
                                                                                                                                                                                                                      494 CAGGIGITITATGGIACAATICCIAAGGGIAGCAGAATIACAGTTATGAAGTGGCGAATGAA 435
                                                                                                                            554 cctricraadagercraacageccaricacagagetescaracageagagecerererer
                                            Gaps
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..2618, 2890..3164, 4291..4509, 4598..4709, 4795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MINATO, Nagahiro
APPLICANT: HATTORI, Masakazu
APPLICANT: HIROSHI, Kubota
APPLICANT: MASATSUGU, Maeda
TITLE OF INVENTION: SPA-1 PROTEIN AND GENE CODING THEREFOR
NUMBER OP SEQUENCES: 7
ADDRESSED: FOLEY & Lardner
                                          40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/895,628
                                                                                                                                                                                                                                                                   351 ATAATTTTATGATTGAAGGTCACCACAACATGAGG 385
                                                                                                                                                                                                                                                                                                             434 AATAATTTTTGA-TCAGGTCACCACACCATGTGG 401
         Best Local Similarity 72.3%; Pred. No. 2.5e-09;
Matches 112; Conservative 0; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/380,403
FILING DATE: 30-JAN-1995
APPLICATION NUMBER: US 08/325,909
FILING DATE: 19-OCT-1994
PROR APPLICATION DATA:
APPLICATION NUMBER: UP 6-279712
FILING DATE: 20-OCT-1994
PROR APPLICATION DATA:
APPLICATION NUMBER: UP 6-139513
FILING DATE: 30-MAY-1994
ATTORNEY/AGENT INPORMATION:
NAME: WEGNER, Harold C
REGISTRATION NUMBER: 25,258
REFERENCE/POCKET NUMBER: 25,258
REFERENCE/POCKET NUMBER: 25,258
TELLEPAN: (202) 672-5300
TELLEPAN: (202) 672-5309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: FOLEY & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington STATE: D.C. COUNTRY: USA ZID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                       US-08-895-628-4/c
; Sequence 4, Application US/08895628
Patent No. 5998885
; GENERAL INFORMATION:
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MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 6645 Dags TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
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Sequence 158, App Sequence 42, App Sequence 62, Appl Sequence 55, Appl Sequence 55, Appl Sequence 52, Appl Sequence 26, Appl Sequence 107, Appl Sequence 115, Appl Sequence 115, Appl Sequence 115, Appl Sequence 31, Appl Sequence 567, Appl Sequence 567, Appl Sequence 567, Appl Sequence 1880, Appl Sequence 31, Appl Sequence 31, Appl Sequence 64, Appl Sequence 31, Appl

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Sequence 1, Application US/10005337A

| Publication No. US20030039964A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: SCHWARTZ, Bertrand
| APPLICANT: BRANBLLEC, Didier
| APPLICANT: CHIEN, Kenneth R. |
| TITLE OF INVENTION: THEM AND USES THEREOF |
| TITLE OF INVENTION: THEM AND USES THEREOF |
| FILE REFERENCE: 03806.0330.00000 |
| CURRENT APPLICATION NUMBER: US/10/005,337A |
| CURRENT FILING DATE: 2001-12-07 |
| PRIOR FILING DATE: 2001-12-07 |
| NUMBER OF SEQ ID NOS: 5 |
| SOSTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GGCTTTGCCACCCATGAATACTTCCTAGTCTAGTCCGTTTGTGAAACTCAGCCCATCCCA 120
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US-10-125-994A-25

US-10-125-994A-26

US-09-124-322B-107

US-09-72B-446-115

US-09-72B-446-115

US-09-72B-446-139

US-09-72B-446-339

US-09-72B-446-339

US-09-72B-446-339

US-09-72B-46-339

US-09-866-050A-567

US-09-867-701-1380

US-09-867-701-1380
US-10-265-071-24

US-09-974-298-182

US-10-240-65-158

US-10-155-21-97-421

US-10-175-523-62

US-10-175-523-62

US-10-084-817-217

US-10-084-817-217

US-10-004-113-55

US-09-923-876-5218
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US-10-044-592-93
US-10-044-592-95
US-09-809-545A-15
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US-10-208-304-6
US-10-003-806-10
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.larity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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Best Local Simi
Matches 2358;
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                                                                                         2003, 03:51:42; Search time 698.036 Seconds (without alignments) 11040.154 Million cell updates/sec
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5: /cgn2_6/ptodata/1/pubpna/USOF_NEW_PUB.scq:*

7: /cgn2_6/ptodata/1/pubpna/USOF_NEW_PUB.scq:*

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9: /cgn2_6/ptodata/1/pubpna/USOF_PUBCOMB.scq:*

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17: /cgn2_6/ptodata/1/pubpna/USOF_NEW_PUB.scq:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-005-337A-2

US-10-175-523-80

US-009-771-208-20

US-10-175-523-97

US-009-771-208-20

US-10-105-503-1

US-10-105-503-1

US-10-175-523-62

US-110-226-188-3

US-10-226-188-3

US-10-226-188-3

US-09-917-800A-477

US-09-917-8445-91

US-09-917-800A-477

US-09-917-8044-183

US-09-917-8044-183

US-09-813-526-183
                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                               2169961 seqs, 1634102185 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                  nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Match
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APPLICANT: Brockman, Jeffrey
APPLICANT: Brockman, Jeffrey
APPLICANT: Evans, David
APPLICANT: Hook, Derek
APPLICANT: Hook, Derek
APPLICANT: Hook, Derek
APPLICANT: Hook, Derek
APPLICANT: Rajan, Michael
APPLICANT: Palfreyman, Michael
APPLICANT: Rajan, Prithi
PRIOR FILING DATE: 2002-06-18
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2002-01-18
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                                                                                                                                 1938 TTACTTCGGTTCCCAGGTTGGAAGATTATCTCACCCCGGCCCCAGCTATATAAGCTGACCG
                                                                                        TGACTTGGCTTCCCAGGCTGGAAGATTATCTCACCCAGCCCTAGCTATATAA-CGGGCTG
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Pred. No. 5.7e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 80, Application US/10175523; Publication No. US20030096264A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.3%;
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; ORGANISM: Mus musculus
US-10-175-523-80
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Best Local Similarity
Matches 139; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1289 rchafrichtgaccachcharccafrificaachaaaahgchccaarharrangchch
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Pred. No. 3.4e-101;
0; Mismatches 162;
                                                                                                                                               Sequence 2, Application US/10005337A
FUBLication No. US20030039984A1
GENERAL INFORMATION:
APPLICANT: BENOIT, Patrick
APPLICANT: SCHWARTZ, Bertrand
APPLICANT: BRANELLEC, Didier
APPLICANT: GRANELLEC, Didier
TITLE OF INVENTION: SEQUENCES USSTREAM OF THE
TITLE OF INVENTION: THEM AND USES THEREOF
TITLE OF INVENTION: THEM AND USES THEREOF
TITLE OF INVENTION: 2030-00000
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/251,582
PRIOR APPLICATION NUMBER: US 60/251,582
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
2341 GGTCGGAGGCCACCATGG 2358
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Best Local Similarity 76.4%;
Matches 597; Conservative 0
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APPLICANT: BYONG, Derek
APPLICANT: BYONG, Derek
APPLICANT: BYONG, Derek
APPLICANT: Klincak, Leazek
APPLICANT: Laeng, Pascal
APPLICANT: Rajan, Michael
APPLICANT: Rajan, Prithi
APPLICANTON NUMBER: US/10/175,523
CURRENT APPLICATION NUMBER: US 60/299,151
PRIOR APPLICATION NUMBER: US 60/299,151
PRIOR PRILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: US 60/317,828
PRIOR APPLICATION NUMBER: US 60/317,828
PRIOR APPLICATION NUMBER: US 60/333,047
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 60/349,936
PRIOR APPLICATION NUMBER: US 60/349,936
PRIOR APPLICATION NUMBER: US 60/340,936
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Pred. No. 6e-1.
0; Mismatches
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                                                                                                                                                                                                                                                 Sequence 97, Application US/10175523
Publication No. US20030096264A1
GENERAL INFORMATION:
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Best Local Similarity 68.8
Matches 130; Conservative
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US-09-771-208-20/c
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Publication No.
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                                                                                                                                       APPLICANT: BRADFORD, ERIC
APPLICANT: HORVAT, SIMON
TITLE OF INVENTION: CLONING OF A HIGH-GROWTH GENE
FILE REFERENCE: 407T-923110US
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 08/999,477
PRIOR APPLICATION NUMBER: US 08/999,477
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
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Pred. No. 8.5e-14;
0; Mismatches 42;
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LOCATION: (123459)...(123478)
OTHER INFORMATION: n is unidentified a, c,
NAME/KEY: misc feature
LOCATION: (602466)...(602485)
OTHER INFORMATION: n is unidentified a, c,
NAME/KEY: misc feature
LOCATION: (546998)...(547017)
OTHER INFORMATION: n is unidentified a, c,
NAME/KEY: misc feature
LOCATION: (494715)...(494814)
OTHER INFORMATION: n is unidentified a, c,
NAME/KEY: misc feature
LOCATION: (330986)...(391005)
OTHER INFORMATION: n is unidentified a, c,
NAME/KEY: misc feature
LOCATION: (330986)...(391005)
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LOCATION: (170625)..(170645)
OTHER INFORMATION: n is unidentified a,
NAME/KEY: misc_feature
LOCATION: (132680)..(132700)
OTHER INFORMATION: n is unidentified a,
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LOCATION: (117174)...(317193)
OTHER INFORMATION: n is unidentified a,
NAME/KEY: misc_feature
LOCATION: (280353)...(280373)
OTHER INFORMATION: n is unidentified a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (271829)..(271848)
OTHER INFORMATION: n is unidentified a,
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LOCATION: (183872)..(183891)
OTHER INFORMATION: n is unidentified a,
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LOCATION: (346860)..(346823)
OTHER INFORMATION: n is unidentified a,
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; OTHER INFORMATION: n is a, c, g, or
US-09-771-208-20
                                                Sequence 20, Application US/09771208 Patent No. US20020155564A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 74.7%;
Matches 139; Conservative
                                                                                              GENERAL INFORMATION: APPLICANT: MEDRANO, JUAN
                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Mus musculus
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LENGTH: 659158
                     -09-771-208-20
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251 CGACCCTTTACAGGGGTCACATATCATCTATATGTCAGGTATTTACATTACGATT 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  441 CAACACCCTTTGGGCGTCCTATATCCGATATCCTGCATATCCAATATTTACATGACGATT 500
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                                                                                                                                                                                                                    APPLICANT: Graff, Jonathon M.
APPLICANT: Muenster, Matthew
TITLE OF INVENTION: METHODS TO IDENTIFY SIGNAL SEQUENCES
FILE REFERENCE: 3.34943 000495.0243
CURRENT APPLICATION NUMBER: US/10/002,631C
CURRENT FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: 60/300,309
PRIOR FILING DATE: 2001-66-21
NUMBER OF SEQ ID NOS: 334
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              w=a or t; y=c or t;
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Pred. No. 1.7e-12;
0; Mismatches 51;
                                                                                                                               ; Sequence 156, Application US/10002631C; Publication No. US20030157486A1; GENERAL INFORMATION:
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LOCATION: (1)...(203)
OTHER INFORMATION: n = A, C, G or T
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; Publication No. US20030167488A1
; GENERAL INFORMATION:
APPLICANT: Roberds, Steven L
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; OTHER INFORMATION: m=a or c;
US-10-195-963-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 101; Conservative
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Best Local Similarity 70.8
Matches 136, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Mus musculus
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ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 156
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US-10-195-963-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      439418 TCTAGACTAGTGGTTCTCAACCTATGGGTTTCAACCTCTTTGGGAGTTTCATATCAGATA 439359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258 TTACAGGGGTCACATATCATCTATATGTCAGGTATTTACATTACGATTCGTAACA 317
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ches 50; Indels
APPLICANT: HORVAT, SIMON
TITLE OF INVENTION: CLONING OF A HIGH-GROWTH GENE
FILE REFERENCE: 407T-923710US
CURRENT APPLICATION NUMBER: US/09/771,208
CURRENT FILING DATE: 2001-01-26
FRIOR APPLICATION NUMBER: US 08/999,477
PRIOR FILING DATE: 1997-12-29
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
SEQ ID NO 20
LENGTH: 659158
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Pred. No. 1e-11
0; Mismatches
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LOCATION: (123459)..(123478)
OTHER INFORMATION: n is unidentified a, c,
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LOCATION: (183872). (183891)
OTHER INFORMATION: n is unidentified a, c,
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LOCATION: (546998)..(547017)
OTHER INFORMATION: n is unidentified a,
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LOCATION: (494715)..(494814)
OTHER INFORMATION: n is unidentified a,
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LOCATION: (390966)..(391005)
OTHER INFORMATION: n is unidentified a,
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LOCATION: (346860)..(346823)
OTHER INFORMATION: n is unidentified a,
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LOCATION: (602466)..(602485)
OTHER INFORMATION: n is unidentified a,
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LOCATION: (317174)..(317193)
OTHER INFORMATION: n is unidentified a,
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LOCATION: (271<u>8</u>29)...(271848)
OTHER INFORMATION: n is unidentified a,
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LOCATION: (280353)..(280373)
OTHER INFORMATION: n is unidentified a,
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; OTHER INFORMATION: n is a, c, g, or t
US-09-771-208-20
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Best Local Similarity 71.8%;
Matches 135; Conservative (
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LOCATION: (170625)..(170645)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             439241 ACATGTGG 439234
                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACATGAGG 385
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Sequence 75, Application US/10228794
Publication No. US20030027198A1
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-228-794-75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 62, Application US/10175523

Publication No. US20030096264A1

GENERAL INPORMATION:
APPLICANT: Brockman, Jeffrey
APPLICANT: Broans, David
APPLICANT: Broans, David
APPLICANT: Laeng, Pascal
APPLICANT: Laeng, Pascal
APPLICANT: Palfreyman, Michael
APPLICANT: Rajan, Prithin
FILE REFRENCE: 3225/10795-US3
CURRENT FILING DATE: 2002-06-18
PRIOR PELLING DATE: 2001-06-18
PRIOR PELLING DATE: 2001-09-07
PRIOR PELLING DATE: 2001-09-25
PRIOR PELLING DATE: 2001-09-25
PRIOR PELLING DATE: 2001-09-25
PRIOR PELLING DATE: 2001-09-25
PRIOR PELLING DATE: 2001-09-15
PRIOR PELLING DATE: 2002-01-18
PRIOR PELLING DATE: 2002-01-18
PRIOR PELLING DATE: 2002-01-18
PRIOR PELLING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 197
SECTION NO 62
                                                                                                                                                                                                                                                                                                    10458 GACAGTAGTAAAATTACAGTTATGCAGTAGCAATGAAAATAATTTTATGGTTGGGGTGAC 10517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55661
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                                                                                       10340 TGCGAGGACAGAGGTTCTCAACCTGTGGGGCACAACCCCTTTGGGG--TTTGAATGACTT 10397
                                                                                                                                                                                               10398 TTCACAGGGGTTGCTTGCCAAAGACCATCAGAAAACACAGGTATTTACATTCCAATTCAT 10457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       322
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                                                                                                                                                                                                                                                314 AACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGAAGGTCAC 373
                                   197 ITCTAGGGCAGCAGTICTCAACCTGGGGGCCTCGACCCCTTTGGGGGAATCAAACGACCC 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263 GGGGTCACATATCATCTATATGTCAGGTATTTACATTACGATTCGTAACAGTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55602 GAGGTCACACATCAGATATCCTCCATATCAAATATTTTACATTATATATTCATAACACTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55662 AAAATTAAAGTTACAAAGTAGCAACAAAATAATTTTATGGTAAGGGGCCATCACAATATG
                                                                                                                                        257 TTTACAGGGGTCACATATCA -- - TCTATCCTATATGTCAGGTATTTACATTACGATTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 185548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 78.2; DB 14;
Pred. No. 6.2e-11;
0; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.3%;
Best Local Similarity 77.2%;
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         10518 CACATCATGAAG 10529
                                                                                                                                                                                                                                                                                                                                                        374 CACAACATGAGG 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    383 AGG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 62
LENGTH: 185548
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RESULT 10 US-10-228-794-75

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177 CICITICAGGATCAGCCTGATICIAGGGCAGCAGTICICAACCTGGGGGCCTCGACCCCT 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239 AATATTTACATTATGATTCATAGTACTACAGAATTACAGTTATGAAGTTACA---AAAT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 TTGGGAGTGCGGTCAAATGACCCTATCACAGGGGTCTCAAATGAGAGATATCCTGCATATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 cacgracaragaragracaaarcragaggacrgrrrrcraraccrgrgagracccr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237 TIGGG----GGAATCAAACGACCCT-TTACAGGGGTCACATATCATCTATCCTATATGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                    Nashville, TN 37240
TITLE OF INVENTION: MAMMALIAN GENES INVOLVED IN VIRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSE: Needle & Rosenberg, P.C.
STREET: 127 Peachtree Street, Suite 1200
CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/228,794
FILING DATE: 27-Aug-2002
CLASSIFICATION: cUnknown>
PRIOR APPLICATION: cUnknown>
PRIOR APPLICATION NUMBER: US/09/171,209
FILING DATE: 08-Mar-1999
APPLICATION NUMBER: PCT/US97/06067
FILING DATE: cUnknown>
ATTORREY/AGRYT INPORMATION:
NAME: Selby, Elizabeth
REGISTRATION NUMBER: 38,298
REFERENCE/DOCKET NUMBER: 22000.0061/P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 78; DB 14;
Pred. No. 1.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         353 AATITIAIGAITGAAGGICACCACAACAIG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           296 AATTTTATAGCTGAGAGTCACCACAACATG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 75:
APPLICANT: VANDERBILT UNIVERSITY
                                                                                                                                                                                                                                                                                              COUNTRY: USA ZIP: 3030-1811
COMPUTER READBLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-10-026-188-3/c
Sequence 3, Application US/10026188
Publication No. US20020164645A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 892 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                           305 Kirkland Hal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 404 688 9880 INFORMATION FOR SEQ ID NO: 75:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 148; Conservative
                                                                                                                                     NUMBER OF SEQUENCES:
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4978 ACTOTAAGCOTGTGGTTCTCAACCCATGAGTCATGACCCTTTGGGATTGTCCAATGACCC 4919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4858 TAACCGTGTCAAATTACAGTTGTGAATAGCAACTAAAATAATTTTGTGGTTTGGGTCA 4799
            ACATATCATCTATCCTATATGTCAGGTATTTACATTACGATTCGTAACAGTAGCAAAATT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           256 CTTT----ACAGGGGTCACATATCATCTATCCTATATGTCAGGTATTTACATTACGATTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313 TAACAGTAGCAAAATTACAGGTATGAAATAGCAATGAAATAATTTTATGATTGAAGGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 ATTICTAGGGCAGCAGTTCTCAACCTGGGGCCTCGACCCCTTTGGGGGGAATCAAACGACC
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US-09-917-800A-477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.2%; Score 75.6; DB 10; Length 5990; Best Local Similarity 66.7%; Pred. No. 3.3e-11; Matches 124; Conservative 0; Mismatches 59; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mendrick, Donna
APPLICANT: Mendrick, Donna
APPLICANT: Donnson, Kory
APPLICANT: Castle, Archur
APPLICANT: Castle, Archur
APPLICANT: Gastle, Archur
APPLICANT: Gane Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US 60/222,040
FRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2001-05-13
PRIOR FILING DATE: 2001-05-15
PRIOR FILING DATE: 2001-05-20
PRIOR FILING DATE: 2001-05-20
PRIOR FILING DATE: 2001-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 477, Application US/09917800A
Patent No. US20020119462A1
GENERAL INFORMATION:
                                                                                                                                                                                                                329 ACAGGTATGAAATAGCA 345
                                                                                                                                                                                                                                                                    319 ACAGTTATGAAGTAGCA 335
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ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              373 CCACAA 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 477
LENGTH: 5990
                                          201
                                                                                                   269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 GTTCTCAACCTGGGGGCCTCGACCCCTTTGGGGGAATCAAACGACCCTTT-ACAGGGGTC 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 GGGGGAATCAAACGACCCTTTACAGGGGTCACATATCATCTATCCTATATGTCAGGTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238539 -- GGAAGTCATATGACCCTTTCAAAGGGCTTGCCTAAGACCATC--AGAAAATAGATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 CTTTCAGGATCAGCCTGATTCTAGGGCAGCAGTTCTCAACCTGGGGGCCTCGACCCCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
TITLE OF INVENTION: No. US20020102543A1e1 Mutated Mammalian Cells and
TITLE OF INVENTION: Animals
FILE REFERENCE: LEX-0102-USA
CURRENT APPLICATION NUMBER: US/09/728,445
PRIOR APPLICATION NUMBER: US 60/168,358
PRIOR PILING DATE: 1999-12-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.3%; Score 76.8; DB 13; Length 249487; 70.2%; Pred. No. 2e-10; ive 0; Mismatches 57; Indels 5; (
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APPLICANT: Zuker, Charles S.
APPLICANT: Zhang, Yifeng
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Assays for Taste Receptor Cell Specific
TITLE OF INVENTION: Ion Channel
FILE REFERENCE: 02307E-114910US
CURRENT APPLICATION NUMBER: US/10/026,188
PRIOR APPLICATION NUMBER: US 60/259,379
PRIOR FILING DATE: 2000-12-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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3.2%; Score 75.8; DB 10;
Best Local Similarity 81.8%; Pred. No. 3.6e-12;
Matches 112; Conservative 0; Mismatches 22;
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                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
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SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. US20020102543A1
GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or G
US-09-728-445-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 70.2'
Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Mus musculus
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LENGTH: 249487
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LENGTH: 335
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or

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Sequence 183, Application US/09901484A.

Sequence 183, Application US/09901484A.

Patent No. US20020119460A1

GENERAL INFORMATION:

APPLICANT: Cohen. Daniel

APPLICANT: Chen. Daniel

APPLICANT: Chumakov, Ilya

TITLE OF INVENTION: Prostate Cancer Gene

FILE REFERENCE: GEN-711AK3D2

CURRENT FILING DATE: 2001-07-09

PRIOR APPLICATION NUMBER: US 08/996,306

PRIOR APPLICATION NUMBER: US 09/218,207

PRIOR FILING DATE: 1998-09-09

PRIOR FILING DATE: 1998-02-22

PRIOR FILING DATE: 1998-02-23

PRIOR FILING DATE: 1999-06-23

PRIOR APPLICATION NUMBER: US 09/318,907

PRIOR APPLICATION NUMBER: US 09/318, 207

PRIOR PLING DATE: 1099-06-23

PRIOR APPLICATION NUMBER: US 09/318, 207

PRIOR PLING DATE: 2001-05-11

NUMBER OF SEQ ID NOS: 578

LENGTH AND 183

LENGTH AND 183
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LOCATION: (616). (616)
NAME/KEY: misc_feature
NAME/KEY: misc_feature
LOCATION: (1552). (1552)
OTHER INFORMATION: n = a, c, g, or t.
NAME/KEY: misc_feature
LOCATION: (2809). (2809)
OTHER INFORMATION: n = a, c, g, or t.
NAME/KEY: misc_feature
LOCATION: (2809). (2809)
LOCATION: (2801). (2824)
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LOCATION: (2831)...(2833)
OTHER INFORMATION: n = a, c, g, or t.
NAME/KEY: misc feature
LOCATION: (2835)...(2835)
OTHER INFORMATION: n = a, c, g, or t.
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OTHER INFORMATION: n = a, c, g,
NAME/KEY: misc_feature
LOCATION: (2828)..(2829)
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OTHER INFORMATION: n = a, c, g,
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OTHER INFORMATION: n = a,
NAME/KEY: misc feature
LOCATION: (2825)..(2826)
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LOCATION: (6247)..(6247)
OTHER INFORMATION: n = a,
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LOCATION: (5259)..(5328)
OTHER INFORMATION: exon 2
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4798 CTACAA 4793
                                                                                      RESULT 14
US-09-901-484A-183
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OTHER INFORMATION: n = a, c, g, or t.
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Patent No. US20020165345A1
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Ilya, Chumakov
                                                                                                or
                                                        OTHER INFORMATION: n = a, c, c
NAME/KEY: misc feature
LOCATION: (8698)..(8698)
OTHER INFORMATION: n = a, c, g,
NAME/KEY: misc feature
LOCATION: (9062)..(9062)
                                                                                                                                                                                                                                                                                                                                                  LOCATION: (12675)...(12791)
OTHER INFORMATION: excn 3
NAME/KEY: misc. feature
LOCATION: (14621)...(14710)
OTHER INFORMATION: excn 4
NAME/KEY: misc. feature
LOCATION: (17578)...(17578)
OTHER INFORMATION: a a, c, g,
NAME/KEY: misc. feature
LOCATION: (17639)...(17639)
OTHER INFORMATION: n = a, c, g,
NAME/KEY: misc. feature
LOCATION: (17639)...(17639)
OTHER INFORMATION: n = a, c, g,
NAME/KEY: misc. feature
LOCATION: (17707)...(17707)
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LOCATION: (12298).(12298)
OTHER INFORMATION: n = a, c,
LOCATION: (12675).(12791)
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LOCATION: (17867)..(17867)
OTHER INFORMATION: n = a, c,
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OTHER INFORMATION: n = a, c,
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MMB/KEY: misc feature
LOCATION: (21789)...(2196.^)
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Best Local Similarity 80.0
Matches 88; Conservative
NAME/KEY: misc feature
LOCATION: (8689)..(869
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US-09-853-526-183
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Score 74.8; DB 10; Length 37950;
Pred. No. 2.2e-10;
0; Mismatches 22; Indels 0;
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: PROSTATE CANCER GENE
FILE REFERENCE: GENEST.13CTOF
CURRENT PAPLICATION NUMBER: US/09/853,526
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 09/338,907
PRIOR FILING DATE: 1999-06-23
PRIOR FILING DATE: 1999-06-23
PRIOR FILING DATE: 1999-06-23
PRIOR FILING DATE: 1998-09-09
PRIOR FILING DATE: 1998-09-09
PRIOR FILING DATE: 1998-09-09
PRIOR FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 578
SOFTWARE: Patent.pm
SEQ ID NO 183
LENGTH: 37950.
TYPE: DNA
ORGANISM: MUM BRICULUS
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Best Local Similarity 80.0%;
Matches 88; Conservative
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LOCATION: 5259..5328
OTHER INFORMATION: exon2
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LOCATION: 12675..12791
OTHER INFORMATION: exon3
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LOCATION: 14621..14710
OTHER INFORMATION: exon4
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LOCATION: 21789..21950
OTHER INFORMATION: exon6
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LOCATION: 23387..23510
OTHER INFORMATION: exon7
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; OTHER INFORMATION: exon8
US-09-853-526-183
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LOCATION: 19822..19912
OTHER INFORMATION: exon5
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9570 Acctarccrectrarcagaractracarrargaarreraacagcagcaaaarcacagraa 9629 276 ATCTATCCTATATGTCAGGTATTTACATTACGATTCGTAACAGTAGCAAAATTACAGGTA 335 336 TGAAATAGCAATGAAATTATTATGATTGAAGGTCACCACAACATGAGG 385 8 d ઠે

9630 CGCAATATCAACAAATAATTTTATGGTTGAGGGCCACCATAACGTGAGG 9679

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Search completed: November 14, 2003, 11:39:40 Job time : 703.036 secs

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Maximum Match 100%
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length: 2000000000
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gb pat: *
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gb v: *
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a .

PAT 16-JUL-2002

linear

DNA

AX468604 2 from Patent W00246220. AX468604 GI:21901403

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 1 AX468604 LOCUS

ALIGNMENTS

Homo sapiens (human) Homo sapiens Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Schwartz, B., Branellec, D. and Chien, K. Sequences upstream of the carp gene, vectors containing them and uses thereof

REFERENCE AUTHORS TITLE

AC119234 Mus muscu AC105469 Rattus no AC097115 Rattus no AR478692 Mus muscu AX322775 Sequence BD094076 Shear str X83703 H.sapiens m G28603 human STS S 422803 JUNEAN 213 S 4X281749 Sequence BV062893 S212P6025 4C026715 Homo sapi AC120060 Rattus no AC095979 Rattus no U73024 Homo sapien AC097718 Homo sapien AC046758 Human DNA AC026471 Homo sapi AC046758 Human DNA AC026471 Homo sapi AC104099 MINE MISCAL AC068946 Homo sapi AC129985 Homo sapi AC090711 Homo sapi AC079993 Homo sapi AC082732 Homo sapi AC084305 Homo sapi AC084305 Homo sapi AX468604 Sequence AF131884 Homo sapi AL365434 Human DNA AC074094 Homo sapi ALS90622 Human DNA AX468603 Sequence AC119234 Mus muscu Homo sapi Homo sapi Homo sapi Homo sapi Homo sapi Rattus no Homo sapi Human DNA Human 1p3 Human 1p3 Homo sapi Human DNA Human DNA Homo sapi Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Human AL365434 1 AC074094 1 AC096394 AL833552 AL390211 | BD093713 | AL358013 SUMMARIES BD094076 HSRNACINP AF131883 AX281749 BV062893 AC026715 AC0120060 AC035979 U73024 AC097718 AC104695 HSJ437M21 AC122863 ALS91291 AC104099 AL365434 AC074094 AL590622 AX468603 AC119234 AC105469 AC068946 AC129985 AC090711 AC079993 AC022732 AC084305 AC137376 0 DB 99.9 2074
667.3 160350
32.1 50111
17.7 22358
17.7 122358
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ATTCCTACGAGTTACCATAAATCAACTCAGAATTCCCTGGAGTGGGGCCAGGGATCTGTA
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Direct Submission

Submitted (21-70N-2002) Wellcome Trust Sanger Institute, Hinxton,

Cambridgeshire, CB10 1SA, UK. B-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Jun 23, 2002 this sequence version replaced gi:12191663.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                             GCCAGTGACATCATAAAAGAAAAGTGCATTACTGAATGCTTTCAATGTCTTATAATGATG
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                                                                                                                               GTAAGGTGGCCATGTCATGGGGCCTATTTAGCCCAGACATCACTCCAAAGAATTCCAAAACA
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                                                                                                                                                                                                  GATATAGACAAGTGCCTTTAGGGCCCCAGATCCCTTCCCCTCAGGCTGTTTACCCCAGGGAA
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together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Bm., BMEL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr10 RPI1-236Bls is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm

VBCTOR: pBACG3.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data of i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Location/Qualifiers
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98.4%; Pred. No. 7.2e-307;
live 4; Mismatches 10;
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	Qy         180         GGCCTGGAACAAAAAGGCATACGAAATGGTAGAAAAAGTGTCCATGACTACTACTTCTGACTT           Db         114819         GGCCTGGAACAAAAAGGCATACGAAATGGTAGAAAAAGTGTCCATGACTACTGACTT	Oy 240 AGATGAAGAGACCAATGAAAATAGTAATGATTGGTTTGGTTCAGCAGGACATATACTAA	OY 300 AATAGGAGCTATACAAAGAAGATTAGCATGGACTCTGTGCAAGAATGACACAAAATTTG	Oy 360 TGAAACATTCCATATTAAAAATAAATAAATAAAGAGAAAAGGAAAAAATTAAAAAA	QY         420 GAAAATAGTGATAGCTGTGTCCCATCTCAAAGAAAAGCCCAGGAGATTTCCTTTATTTA	Qy 478 CCCCTTTAAGATATATTAGGAGACCGGAACATATGATACAGAGGGGGGGG	Qy         538         TCCCTCTTTGTCAAGTTTTTGTCTTGGGGGGAGTCGATGTCTTCTCAAAGTTTCAGA           Db         114459         TCCCTCTTTGTCAATGTTTTGTCTTGGGGGGGGGGGGGG	Oy 598 AACACCATCCACTGACTGAGGGGGAAGAGGAGAATGGCAGCCACATTTGTTG	Qy 658 ATTGGGTGAGTTTGGGGAGAAATAGACACAAAAGGTCAAACATAACTTCCTAATTAACA	QY         718 CTTCCCTCCATTCACAATTCCCTTCTCCCATTCTCTCTC	Oy 778 CCCAGITITICCIGAAACTAIAAAAAIACCCCCAGIAIGITIACAIAAATITACACCCCAA DI 114219 CCCAGITITICCIGAAACTAIAAAAAAGACC-CCAGIAITITIACAIAAAAATITACACCICCAA DD 114219 CCCAGITITITICCIGAAACTAIAAAAAAAAAAAAAAAAA	QY         838 AGATTAGABACCAGABATAGAGACC-TTITCAACCCTTCCGGAAGCAAAGTGCATTATCC           DD         114160 AGATTAGABACCAGABATAGAGACCTTTTCAACCCTTCCGGAAGCAAGTGCATTATCC	Qy         897 CICCAGCCACGTGTCTCAAATCTTGATGCATCAGAATCATGGGGGGTGCTTTKAAATTCAA	957	. · · ·	GCATT 59 Db 113920	
113398 113497: gap of un 113498 141732: contig of	141733 141832: gap of unknown 141833 143187: contrig of 1355 143188 143287: gap of unknown 143288 144942: contrig of 1655 b	144943 145042: gap of unknown 145043 147286: contig of 244 k 147287 147386: gap of unknown 147387 150852: contig of 3466 k	~ 14 ~ 14 ,	157258 157357; gap of unknown length 157358 160350; contig of 2993 bp in l Location/Qualifiers 1160350	/organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="10"	/clone="RP11-236B18" feature 1236 /note="aesembly_name:Contig10" feature 24277519	/note="assembly_name:Contigl1" feature 7620. 12286 /note="assembly_name:Contigl2" feature 1538723050	/note="assembly_name:Contigl3" feature 23151. 33653 /note="assembly_name:Contigl4" feature 3376450133	/note="assembly_name:Contig15" misc_feature 50234. 56088 /note="assembly_name:Contig16" misc_feature 68189. 88133	o o	/noce="assemb1y_name:Contig19" feature 141833. 1.143187 /noce="assemb1y_name:Contig3" feature 143288144942	/note="assembly_name:Contig4" feature 145043. 147286 /note="assembly_name:Contig5" feature 147387. 150852	/note="assembly_name:Contig6" feature 150953. 153550 /note="assembly_name:Contig7" feature 153651. 157257	/note="assembly_name:Contig8" feature 157358. 160350 /note="assembly_name:Contig9" 47390 a 32724 c 33135 g 45498 t 1603 others	Length	2; CONSELVATIVE 4; M.SMATCR CTGCAGCAAGTTACTTAATGTTT-TTTGCC TTGCAGCAAGTTAATGTTTT-TTTTGCCT	09

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24717. .24796,28974. .29381)
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KDSTMRRYTISSALNIMQICKGKNVIISSAAERPLEIRGPYDVANLGLLFGLSESDAK
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join(391. 4772,3273. 3328,3362. 4018,4428. .4502,7467.
14216. .1430,23179. .23295,23858. .23887,24284. .24321,
24717. .24796,28974. .29083)
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/note="match: proteins: Tr:P78346 Tr:O88796"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="bA320F15.1.1 (ribonuclease P (30kD) (RPP30))"
/note="match: cDNAs: Em:U77665 Em:AK004137 Em:U95123
match: ESTS: Em:BE572689 Em:BE378859 Em:BE137893
Em:AA920575 Em:BG106820 Em:BF681617 Em:BF248001
Em:BP031745.Em:AA854455 Em:A1359795"
VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone RP11-320F15 It may be shorter because we sequence overlapping sections only once, except for a short overlap.
The true left end of clone RP11-236B18 is at 50012 in this sequence. The true right end of clone RP11-103A2 is at 100 in 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .2502 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .2696 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAVSTNCRAALLHGETRKTAFGIISTVKKPRPSEGDEDCLPASKKAKCEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="MIR repeat: matches 30. .132 of consensus"
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/note="match: ESTs: Em:AW939965"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (4176. .4649)
/note="match: GSS: Em:AQ626500"
join(<4648. .4764,7467. .7538,14216. .14308,24284. .24331,24717. .24796,28974. .29381)
/gene="bA320815.1"
                                                                                                                                                                                                                                                                                                                                                                                        /Clone="RP11-320F15"
/Clone_lib="RPCI-11.2"
complement(1. .98)
/Clote="match: GSS: Em:AQ670367"
complement(1. .97)
/note="match: GSS: Em:AQ544636"
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/note="L2 repeat: matches 2557.
2939. .3167
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1926. .2208
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                                                                                                                                                                                                                                         1. .50111
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                       type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                db_xref="taxon:9606"
chromosome="10"
                                                                                                                                                                                                                Location/Qualifiers
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/note="match: STS:
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'qene="bA320F15.1"
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'gene="bA320F15.1"
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/note="L2 re
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On May 31, 2001 this sequence version replaced gi:14161205.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-effranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least one plasmid subclone or more than one Mills subclone; and the
                                                                                          CCTAAGCTAAGCAATCTTCCTGTCTCTGCCTCCCAAAATGTTGGGATTACAGGTGTAAGC 113741
                                                                                                                                                                                                                                         113621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL590622 50111 bp DNA linear PRI 19-SEP-2001 Human DNA sequence from clone RP11-320F15 on chromosome 10. Contains the gene for ribonuclease P 30kD subunit, the gene for a nuclear protein similar to CARP, BSTs, STSs and GSSs, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (19-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                      113680 TIGAAGTAAAAATGCTCCAATTATTATGCTGTTTTAGAACACGGTAAGCATGTCCATGTGC
                                                                                                                                                                                                                                                                                                 1376 TA---ATGGCCAGTGACATCATAAAAGAAAAGGAAAGTGCATTACTGAATGCTTTCAATGTCTTA
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                                                           CACTGCACCCGGCTGATAGCTGGTTTCATTTACTCTATTTCTTGACCACTCTGATCCATT
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HTG; CARP; ribonuclease P.
Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                         Gaps
                                                         50111;
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                                           .6302
                                                                                                                                                            Length
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                                           repeat: matches 5888.
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                                                                                                                                                            Score 664.8; DB 9;
Pred. No. 9.2e-141;
complement (25417. .25863)
/note==match: GSS: Em:AQ712354"
26204. .26603
/note=="LIMA2 repeat: matches 588
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Mus musculus
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                                                                                     29149. .29154
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Best Local Similarity 99.6%;
Matches 677; Conservative (
                               repeat_region
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join(23179. .23295,23858. .23887,24284. .24321,24717. .24796,
28974. .29072,30647. .30748,31596. .31680,33706. .34469)
/gene="bA320F15.1"
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/note="march: EST915: Em:BE567341 Em:A1292002 Em:BF684192
Em:BR435407 Em:A1740881 Em:AA651912 Em:BF438915"
/evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="1105x repeat: matches 45. .304 of consengus"
19198. .19363
/note="LIME repeat: matches 5272. .5435 of consensus"
19489. .199189
/note="MLTIC repeat: matches 5. .478 of consensus"
21838. .2258
/note="L2 repeat: matches 2109. .2669 of consensus"
22440. .22946
/gene="bA320F15.1"
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/note="match: GSS: Em:B53566"
25321. .25458
/note="FLAM_C repeat: matches 1. .133 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="Alujo repeat: matches 1. .282 of consensus"
15791. .16088
note="AluSg repeat: matches 1. .296 of consensus"
16979. .17036
"hote="L2 repeat: matches 2423. .2481 of consensus"
7236. .17755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="match: GSS: Em:AQ026750"
complement(join(24284. .24321,24724. .24796,28974.
/note="match: STS: Em:G24365"
                              .2732 of consensus"
                                                                                                                              722. .6237
note="L2 repeat: matches 1200. .1808 of consensus"
                                                                                                                                                                                    note="FLAM C repeat: matches 1. .129 of consensus" 1319. .114\overline{9}1
                                                                                                                                                                                                                                                                                                                                                                                                                                     note="L2 repeat: matches 1743. .1801 of consensus" 3755. .13817
                                                                                       consensus,
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                                                            consensus,
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1928. .11984
                                                                                                                  .293 of consensus"
                                                                                                                                                                          .312 of consensus"
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                                                          .2478 of
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/evidence=not_experimental
4733. .4858
4733. .4858
7 note="12 repeat: matches 2599. .7
7 note="12 repeat: matches 2299. .7
7 note="12 repeat: matches 1808. .1
7 note="12 repeat: matches 1808. .1
                                                                                                      440. .5721
note="AluSx repeat: matches 7.
                                                                                                                                                            s884. .7196
/note="AluJb repeat: matches 1.
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5390. .15671
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24561, .24956
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1086. .11219
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.7709. .17972
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Larna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Colline, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dawar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindelad, Toh, K., Liu, G., MacLean, C., Macdonald, P., McKernan, K., Major, J., Marquis, N., Mathews, C., MacLean, C., Macdonald, P., McKernan, Y., Major, J., Naylor, J., Naylor, J., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Schupback, R., Schupback, R., Schupback, R., Schuper, S., Severy, P., Spance, M., Riley, R., Schuuer, S., Studer, J., Sancos, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, M., Travis, M.,
                                                                                                                                                            DNA linear HTG 11-JUN-2003
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                             Schwartz,B., Branellec,D. and Chien,K.
Sequences upstream of the carp gene, vectors containing them and
uses thereof
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Aventis Pharma S.A. (FR) ; The Regents of The University
California at San Diego (US) ; Benoit, Patrick (FR)
Location/Qualifiers
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I (Dases I to 229940)

Muzny, D. Marie., Alsorbooks, S., Amin, A., Anguiano, D., Alder, J., Allon, H., Alsbrooks, S., Amin, A., Anguiano, D., Angualabechi, V., Aoyagi, A., Ayodej, M., Baca, B., Baden, H., Balom, H., Baladaranaike, D., Barbber, M., Barnstead, M., Benahmed, F., Bindin, D., Barbber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blath, F., Brown, M., Bryant, M., Charter, J., Chavezo, I., Ceasar, H., Cener, A., Chavezo, C., Corlen, R., Chen, Y., Chen, Z., Chu, J., Chavezo, D., Chen, R., Caraco, Chen, R., Chen, Y., Chen, Z., Chu, J., Chavezo, D., Chen, R., Corkell, R., Cox, C., Coyle, M., Cree, A., Dederich, D., Delgado, O., Denson, S., Duramo, C., Ding, Y., Dinh, H., Dinya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Esocto, M., Bugene, C., Brante, C., Faraer, C., Ranies, M., Garcia, A., Garrer, M., Enger, P., Fraaer, C., M., Cabie, A., Hander, C., Porter, M., Gebregeorgis, E., Geer, K. Gill, R., Grady, M., Guevara, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guevara, M., Handers, C., Havlak, P., Hawe, Y., Havlak, P., Hawel, Y., Handle, M., Hamilton, C., Hamilton, K., Harler, M., Mahindartne, M., Mahindartne, M., Mahindartne, M., Mahindartne, M., Martin, K., Martin, R., Martin, K., Martin, R., Martin, K., Martin, R., Martin, K., Martin, R., Ma
                                                                                                                                                                                                                                                                                                                                                                                         AC105469 229640 bp DNA linear HTG 15-NOV-2002
Rattus norvegicus clone CH230-140118, WORKING DRAFT SEQUENCE, 9
CCTGATTCACATATTCAGCAGGGTTAGCTTGTCCTCCCCTCCTCCAGCTTCCCCAGAC 1877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                              91380 CCTGATTCGCATACGCCGCGG-----CCAGCTTGTCATCTCCCTCTTGGGCTTCCCAGAC
                                                                                                                                                                                                                                    TTACTTCGGTTCCCAGGTTGGAAGATTATCTCACCCGGCCCCCAGCTATATAAGCTGACCG
                                                                                                                                                                                                                                                                     1998 GTGTGGAGGGCCCAGCAGGGCCAACTCCAGGGATTCCTTC-CACGACAGAAAAACATAC
                                                                                                                   AC105469.4 GI:25007338
HTG; HTGS PHASB1; HTGS_DRAFT; HTGS_FULLTOP
Rattus norvegicus (Norway rat)
Rattus norvegicus
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AC105469
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                                                      * NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.

1 6126: contig of 6126 bp in length
6127 142902: contig of 81676 bp in length.
Location/Qualifiers
1. 142902

/roganism="Wuss musculus"
/mol_type="genomic DNA"
/don_type="genomic DNA"
/clone libe=RRP24-211P24"
/clone libe=RRP24-211P24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90844 TCTCTCTGTGCATCACTTCGGCCCGTTTTGGGGT--AGATCCTCTGATTAGCCTTCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1349 TTAGAACACGGTAAGCATGTCATGTGCTA---ATGGCCAGTGACATCATAAAAGAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11022 TTTAGCTGCAGACATCACTCCAGAGAATTCCAAACAGATAGAGACAAGTGGCACCCAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 142902;
   Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 367.8; DB 2;
Pred. No. 3.2e-73;
0; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 76.4%;
Matches 597; Conservative
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BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission of Molecular and Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:23101653.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.ltm.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Snedd, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Strong, X., Sutton, A., Svatek, A., Tabor, P., Taylor, P., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vara, V., Villasana, D., Waldron, L., Walker, B., Wang, C., Willson, S., Warren, R., Weider, K., White, F., Willson, R., Wleczy, R., Wooden, H., Worley, K., Wight, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weise, R., Smith, D.R., Holt, R.A., Smith, H.O., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (09-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 229640)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assembly program: Phrap, version 0.990329
Consensus quality: 215126 bases at least Q40
Consensus quality: 217436 bases at least Q30
Consensus quality: 218866 bases at least Q20
Estimated insert size: 214300; sum-of-contigs estimation
Quality coverage: 10x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: hgsc-help@bcm.tmc.edu
------ Project Information
Center project name: GNAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 229640)
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215567: g
218782: c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1289 TCTATTTCTTGACCACTCTGATCCATTTTGAAGTAAAATGCTCCAATTATTATGCTGTT
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161 223160: gap of unknown length 224771: contig of 1611 bp in length 772 2248771: gap of unknown length 225886: contig of 1015 bp in length 887 225886: gap of unknown length 987 225886: gap of unknown length 1881 228280: gap of unknown length 1881 228640: contig of 2194 bp in length 1881 226640: contig of 1360 bp in length Location/Qualifiers
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                                                                                                                                                                                                                                                                          organism="Rattus norvegicus"
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clone_end:T7"
215568. .216791
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complement(7251. 8156)
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                                                                                                                  141847 GCAGCGATGTGGTGCAATATGAACAGGCAGCTGTCCCTGGCTTCCCGATAAGTAGGATGA 141906
                                                                                                                                                                                                                                                              142082 TTGGCTTCCCAGGCTGGAAGATTATCTCACCCAGTCCTAGCTATATAAG-AGGCTGGGGT 142140
                                                                                                                                                                                                                                                                                                                                                                                                                                    1762 CTTGCATTGCTGAGCGATGTGATCACCACCAAAGGAATGGCCCTTCACATTTCTTCCTG 1821
                                                                                                                                                                                                                      1942 TTCGGTTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATATAAGCTGACCGGTGT 2001
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*** SEQUENCING IN PROGRESS ***,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002 GGAGGGCCCAGCAGGCCAAGACTCCAGGGATTCCTTC-CACGACAGAAAACATACA 2057
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Rattus norvegicus clone CH230-26A2,
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HTG; HTGS_PHASE1; HTGS_DRAFT; F
Rattus norvegicus (Norway rat)
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Direct Submitted (14-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Daylor Plaza, Houston, TX 77030, USA

On Nov 14, 2002 this sequence version replaced gi:22855482.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.ed/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, B., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valex, R., Valex, V., Villasana, D., Waldron, L., Walker, B., Wang, C., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R., Folt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (11-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 238344) (bases 1 to 238344) Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 236546: contig of 236546 bp in length 236547 236646; gap of unknown length 236447 238144: contig of 1698 bp in length. Location/Qualifiers
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Contact: hgsc-help@bcm.tmc.edu
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1352 GAACACGGTAAGCATGTCATGTGCTA---ATGGCCAGTGACATCATAAAAGAAAGTGCA 1408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1588 AAGTGAAGTGTTGATAAGTCTGCTTATCAGAAAGATATTACTGGGGGTGTGATATGTAGG 1647
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 AACTGGATGCGTATAAGTCCAGTTATCAGAAAGATATGGCTGTAAGTGTGATCGACAGT
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                                           Macda T. Sepulveda, J. Chen, H. H. and Stewart, A.F.R.
Alphal-Adrenergic activation of the cardiac ankyrin repeat progene in cardiac mycoytes
Gene 297 (1-2), 1-9 (2002)
Adeada T. Sepulveda, J. and Stewart, A.F.R.
Direct Submission
Submitted (29-JAN-2002) Cardiovascular Institute, University, Pittsburgh, 200 Lobrop Street, Pittsburgh, PA 15213, USA
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Pred. No. 5.2e-67;
0; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                          UTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="Carp"
/codon_start=1
/product="cardiac ankyrin repeat pr
/protein_id="AALB5342.1"
/db_xref="G1:19110907"
a 185 c 180 g 171 t
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="FVB"
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                                                                                                                                                                                                                                                             TTAGAGCAC----ATGCCATGCACTAATTATGGCCAGTGACACCATAAAGTAAAAGTGCA
                                                                                                                                                                                                                                                                                                                         ----CTTCCCCCCGGGCTGTTATTCCCAGGAATAGGATGTCCCAAAGCAACCTTCCA
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                                                                                                                                              Gaps
                                                                                                                                              26;
                                                                                                              Length 238344;
                                                                 6855 others
                                                                                                           17.6%; Score 365; DB 2; Length 23 llarity 77.3%; Pred. No. 1.4e-72; Conservative 0; Mismatches 150; Indels
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                                                              71429
/db_xref="taxon:10116"
/clone="CH230-26A2"
                                             /note="wgs_contig"
47381 c 49225 g
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                                 misc feature
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1901)
Sakurada, K., Kuga, T., Sekine, S., Nakamura, Y. and Sugan, S.
Sakurada, K., Kuga, T., Sekine, S., Nakamura, Y. and Sugan, S.
Shear stress-responsive DNAs 7 12-APR-2001;
KYOWA HAKKO KOGYO CO LTD, HIROSHI NOJIMA, HAJIME YOSHISUE, MASAYA OBAYASHI, TOSHIO OTA, PATKO KAWABATA, KAZUHIRO SAKURADA, TETSURO KUGA, SUSUMU SEKINE, YUSUKE NAKAMURA, SUMIO SUGANO
OS HOmo Gapiens (Human)
                                                                                                                                                                                                                     12-APR-2001
02-OCT-2000 WO 2000JP006840
01-OCT-1999 JP 99P 280976
HIROSHI NOJIMA, HAJIME YOSHISUE, MASAYA OBAYASHI, TOSHIO OTA, PI
                                                                                                                                                                                                                                                                                                   KAZUHIRO SAKURADA, TETSURO KUGA, SUSUMU SEKINE, YUSUKE NAKAMURA, SUMIO SUGANO
CIZNIS/12, CO7K14/435, CO7K16/18, C12P21/02, C12Q1/68, A61K38/00,
A61K39/395,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ankyrin-like repeat; nuclear localisation signal; nuclear protein.
Homo sapiens (human)
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Identification and characterization of a novel cytokine-inducible
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Pred. No. 2.3e-41;
0; Mismatches 5; Indels
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Location/Qualifiers
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/organism="Homo sapiens"
/nol_type="genomic DNA"
/db xref="taxon:9606"
a 378 c 460 g 471
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97.6%;
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Eukaryota; Metazoa;
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Matches 242; Conservative
                                                                                                                                                                                                                                                                                    AYAKO KAWABATA,
PI KAZUHIRO SAKI
PI SUMIO SUGANO
PC C12N15/12, C7
PC A61K39/395,
PC A61K48/00, A6
FH KEY
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                                                                                                                                                          595 TTCCCAGGCTGGAAGATTATCTCACCCAGCCCTAGCTATATAA-CGGGCTGGTGGAGG
                                                                                                      CATATTCAGCAGGGTTAGCTTGTCCTCCCCTCCTCTTCAGCTTCCCAGACACTGAGTCT
                      TTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATATAAGCTGACCGGTGTGGAGG
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Pred. No. 2.3e-41;
0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bunk, D., Reuner, B., Beck, J. and Henkel, T.
Novel target genes for diseases of the heart
Patent: WO 0192567-A 19 06-DEC-2001;
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AX322775
AX322775.1 GI:18093755
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WO 0125427-A/37.
Homo sapiens (human)
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Best Local Similarity 97.6%;
Matches 242; Conservative
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AX322775
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Euteleostomi;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prepared with primer pairs provided by Sandoz, derived from X83703
-- Washington University/Merck EST sequence.
Location/Qualifiers
1. .1901
/ Organism="Homo sapiens"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 1901)

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23 seconds
30 seconds
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Pred. No. 2.3e-41;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                   94 degrees C for 15
62 degrees C for 23
72 degrees C for 30
30
Perkin Elmer 9600
                                                                                                                                         Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford,
Tel: 4157259687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         each 1 uM
each 200 uM
0.05 units/ul
10 ul
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                                                                                                                                                                                                                                                                                Primer A: GGCATTTTGAAGGCATGG
Primer B: CCAGATGGATGATCATGAAGG
                                                                                                                                                                                                                                            Email: myers@shgc.stanford.edu
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/map="10"
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Annealing:
Polymerization:
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Taq Polymerase:
Total Vol:
                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR Cycles:
Thermal Cycler:
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97.6%;
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        Homo sapiens (human)
                                                                                      Myers, R.M.
Unpublished (1996)
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Best Local Similarity 97.6
Matches 242; Conservative
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Tris-HCl:
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PCR Profile:
                          Homo sapiens
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primer_bind
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LKTLLAHPVTLGEQOWKSEKQREAELPKKKLEQRSKLENLEDLEIIIQLKKRKKYRKT
KYPVVKKEPEEPEIITEPVDVPFLKAALENKLPVVEKFLSDKNNPDVCDEYKRTALHRA
CLEGHLAIVEKLMEAGAQIEPRDMLESTAIHWASRGGNLDVLKLLLNKGAKISARDKL
LSTALHVAVRTGHYEGABLIACEABLIANDREGDTPLHDANRLNRYMIRLINYGA
DLNIKNCAGKTPMDLVLHWQNGTKAIFDSLRENSYKTSRIATF"
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                                                                 2 (bases 1 to 1901)
Chu,W.
Chu,W.
Direct Submission
Submitted (05-JAN-1995) W. Chu, Hoffmann-La Roche, 340 Kingsland
Street, Dept. of Inflammation/Autoimmune Disease, Hoffmann-La
Roche, Nutley, NJ 07110, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATATAAGCTGACCGGTGTGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                  250. .1209
/note="cytokine-inducible expression"
nuclear protein from human endothelial cells J. Biol. Chem. 270 (17), 10236-10245 (1995) 95247734
                                                                                                                                                                                                                                                                                                                                                                                   signal"
                                                                                                                                                                                                                                                                                                                                                                 94. .98
'note="nuclear localization
                                                                                                                                                                                                                                                                                                                                                                                                 .52. .283
'note="ankyrin-like repeats'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="nuclear protein"
/protein_id="CAA58676.1"
/db_xref="G1:793841"
/db_xref="SPTREMBL:Q15327"
                                                                                                                                                                                      1. :1901
/organiam="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/chromosome="10"
                                                                                                                                                                                                                                                                                          /cell_type="endothelial"
/tissue_type="skin"
/clone_lib="HDMEC_cDNA"
1. .1901
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Matches 242; Conservative
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                                                                                                                                                                                               Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
(Lases 1 to 1940)
Aihara,Y., Kurabayashi,M., Arai,M., Kedes,L. and Nagai,R.
Molecular cloning of rabbit CARP cDNA and its regulated expression in adriamycin-cardiomyopathy
Eliochim. Biophys. Acta 1447 (2-3), 318-324 (1999)
                                                                                                                                                                                                                                                                                                                                                                   10542334
2 (bases 1 to 1940)
Aihara, Y.

Direct Submission
Submitted (26-FEB-1999) Second Department of Internal Medicine,
Gunma University School of Medicine, 3-39-15 Showa-machi, Maebashi
371-8511, Japan (1971): 1972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ACTGGCAGGGGCAGGCTGTTACTTGGGTTCCCAGGTTGGAAGATTATCTCACCCAGC 120
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7.4%; Score 154.4; DB 4; Length 1940;
Best.Local Similarity 84.9%; Pred. No. 1.3e-24;
Matches 185; Conservative 0; Mismatches 31; Indels 2;
                                                                    1940 bp mRNA linear Oryctolagus cuniculus CARP mRNA, complete cds. AF131883 AF131883.1 GI:6478316
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1. 1940
/ Organism="Orytcolagus cuniculus"
/mol_type="mRNA"
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219- 1178
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           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Database

Result No.

D-amino acid

immune/haema

immune/haema

New promoter sequence derived from a portion upstream of the coding sequence of a gene for Cardiac Ankyrin Repeat Protein, for controlling the level and specificity of expression of a transgene in cardiac muscle cells

2; 48pp; English Fig 5; Claim

The invention relates to a polynucleotide (I) comprising a fragment of a sequence upstream of the coding part of the gene for the Cardiac Ankyrin Repeat Protein (CARP). (I) is capable of inducing a specific expression in vivo of a gene operably linked to (I), in cardiac cells. (I) or a vector (IIb) comprising (I) is useful for the manufacture of a medicament in enterded for the treatment of cardiac insufficiency, cardiac hypertrophy and hypoxia, and for preventing rejection during cardiac transplant. An expression cassette under the control of (I) is useful for encoding a protein or RNA which is capable of activating the growth of cardiac cells, reducing or suppressing an immune response, inducing angiogenesis, correcting muscle contractility, cardiac hypertrophy, cardiac correcting muscle contractility, cardiac hypertrophy, cardiac fletchency and myocarditis. (IIb) is useful for expressing a gene of the rangentic interest in vivo, by isolating (IIb) and introducing (IIb) in the cardiac tissue, under conditions so that the gene of interest is caparimental, therapeutic and diagnostic fields, and in the treatment and prevention of cardiac pathologies. (I) is also useful for generating transgenic animals which constitute models for studying certain cardiac perhologies. (I) is also useful for screening concluding the CARP protein. The present sequence represents the DNA fragment upstream of the coding sequence of a human CARP protein. 

Seguence 2074 BP; 612 A; 469 C; 416 G; 572 T; 5 other;

ö 300 300 360 480 480 540 180 180 240 240 360 420 420 900 120 GTCTTGCTCCAACTTCGAGGGCATGGACAGCTCTGGGATTTCATATCCAAGACCCTTAAA 120 9 CTGCAGCAAGTTACTTAATGTTTTTTTGCCTCAGCATCCTCTGTAAAATGAGAGCATTA GATGAAGAGACCAATGAAAATAGTAATGACTCTGTTTGCTTCAGCAGGACATATACTAAA CTCTTTGTCAATGTTTTGTCTTGGGGTGGGGAGTCGATGTCTTCTCAAAGTTTCAGAAAC GCCTGGAACAAAAGGCATACGAAATGGTAGAAAAAGTGTCCATGACTACTTCTGACTTA GCCTGGAACAAAAAGGCATACGAAATGGTAGAAAAAGTGTCCATGACTACTTCTGACTTA GATGAAGAGACCAATGAAAATAGTAATGACTCTGTTTGCTTCAGCAGGACATATACTAAA ATAGGAGCTATACAAAGAAGATTAGCATGGACTCTGTGCAAGAATGACACAAATTTGT GABACATTCCATATATABABATABATABATABATABAGGABABAGGABABATTABABAG GTCTTGCTCCAACTTCGAGGGCATGGACAGCTCTGGGGATTTCATATCCAAGACCCTTAAA ATAGGAGCTATACAAAGAAGATTAGCATGGACTCTGTGCAAGAATGACACACAAATTTGT CCTTTAAGATAGAATATTAGGAGACCGGAACATATGATACAGGAGGTACTGGGAGGGTCC CTGCAGCAAGTTACTTAATGTTTTTTGCCTCAGCATCCTCTCTGTAAAATGAGAGCATTA Gaps 24; Length 2074; .; 0 Indels .; 0 DB Query Match 99.9%; Score 2071.6; Best Local Similarity 100.0%; Pred. No. 0; Matches 2074; Conservative 0; Mismatches 121 241 241 301 301 361 361 421 481 541 61 61 121 181 181 421 481

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thended for the treatment of cardiac insufficiency, cardiac hypertrophy and hypoxia, and for preventing rejection during cardiac transplant. An expression cassette under the control of [1] is useful for encoding a protein or RNA which is capable of activating the growth of cardiac cassette under the control of [1] is useful for encoding a protein or RNA which is capable of activating the growth of cardiac cassette under the contractility, cardiac hypertrophy, cardiac hypertrophy, cardiac chrappettic interest in vivo, by isolating (IIb) and introducing (IIb) in the cardiac tissue, under conditions so that the gene of interest is caperismental, therapeutic and diagnostic fields, and in the treatment and prevention of cardiac pathologies. (I) is also useful for generating transgenic animals which constitute models for studying certain cardiac pathologies. (I) is also useful for screening concluding the casses animals are also useful for screening modernologies. The transgenic animals are also useful for screening concluding the CARP protein. The presents enquence represents the DNA. Exagnent upstream of the coding sequence of a mouse CARP protein.
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                                                        GACTCTTGACAAATAGGATGACTTGCATTGCTGAGCGATGTGATCACCACCAAAGGAATG
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                                                                2250 GTGTGGAGGGGCTCCACAGGGCCCAGTTCCAGGGGTTCATCCACAAGAGAAAAACATAG 2309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human type-5 recombinant adenovirus vector used for targeted gene therapy for heart disease and evaluating gene function contains a tissue-restricted promoter and inverted terminal repeat sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine cardiac ankyrin repeat protein (CARP) promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.6%; Score 322.6; DB 21; ilarity 76.3%; Pred. No. 2.5e-65; Conservative 0; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; Page 29-30; 33pp; English.
                                                                                                                                                                                                                                                                                                                                       AAA10406 standard; DNA; 2247 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                        A 2057
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Matches 567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                 AAA10406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cardiac cardiac
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1828 ATATTCAGCAGGGTTAGCTTGT-CCTCCCCTCCCTTCAGCTTCCCAGACACTGAGTCT 1886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 TTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATATAAGCTGACCGGTGTGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 GGAATGAAAATTCACCTGCCTCTGAGTTGGCTCCTAATGGGGGTGGGAGTGTTACTTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1947 TTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATATAAGCTGACCGGTGTGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AAAAACAGCAGGGTTAGCTTGTCCCTCCCCTCTTCAGCTTCCCAGACACTGATTCT
                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of a number of human shear stress reagonse proteins. These are useful in diagnosis, treatment and screening of vacular diseases caused by arteriosclerosis, including heart failure, post-PTCA restenosis and
                                                                                                                                                                                                                                   sequences, proteins encoded by them and antibodies against tell in diagnosis and treatment of vascular disease caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1901;
                                                                                                        Kawabata A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1901 BP; 592 A; 378 C; 460 G; 471 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human CAA58676 protein encoding EST clone X83703 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 228; DB 22;
Pred. No. 2.8e-43;
0; Mismatches 5;
                                                                                                      M, Ota T,
Sugano S;
                                                                                                                                                                                                                                                                                                                        Claim 20; Page 422-425; 678pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
250..1209
/*tag= a
                                                                                                        Obayashi
                                                                                                      H, Obayashi
Nakamura Y,
                                          KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     uvery match
Best Local Similarity 97.6%;
Matches 242; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD27217 standard; DNA; 1901
99JP-0280976.
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                                                                                                  AH, Yosur.
T, Sekine S,
                                                                                                      Yoshisue
                                                                                                                                                                  WPI; 2001-266308/27
                                                                                                                                                                                                                                                                             arteriosclerosis -
                                                              NOJIMA H
                                                                                                                                                                                         P-PSDB; AAB90787
01-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypertension.
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                                        KYOM )
                                                                                                                            Kuga T,
                                                                                                    Nojima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2066
                                                                                                                                                                                                      The invention relates to human polynucleotides (AAI79941-AAI99841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymperides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, acg. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     printed
                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent did not form part of the printer specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATATAAGCTGACCGGTGTGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1828 ATATTCAGCAGGGTTAGCTTGT-CCTCCCTCCCTCTTCAGCTTCCCAGACACTGAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATATAAGCTGACCGGTGTGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                  isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22; Length 1988;
                                                                                                                                                              Claim 1; SEQ ID NO 13568; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           stress-response protein; vascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human shear stress-response coding sequence SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1988 BP; 632 A; 384 C; 472 G; 500 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.2e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.1%; Score 229.6;
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Matches 243; Conservative
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               WPI; 2001-514838/56
                                        P-PSDB; AAO13577
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                                                                                                                                                                                                                                                                                                                                                                                                                            inflammation
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The present invention relates to the isolation of human polynucleotide sequences that are differentially expressed during foam cell differentiation. The polynucleotide sequences of the invention or a composition comprising these polynucleotides are useful as a high throughput method for detecting altered expression of one or more polynucleotides in a sample. The polynucleotides can be used in the diagnosis of disorders associated with foam cell development such as a therosclerosis, cerebral stroke, and cardiovascular disorders such as coronary artery disease. The polynucleotide sequences can also be used as PCR primers and probes. The polynucleotide sequences can also be used useful in gene therapy. AAS94746-AAS95021 represent the human polynucleotide sequences of the invention are also polynucleotide sequences of the invention which are differentially expressed during foam cell differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Composition useful for diagnosis of conditions, disorders or diseases associated with atherosclerosis, comprises several polynucleotides that are differentially expressed in foam cell development -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Porter GJ, Mikita T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1929 GCGGGAGTGTTACTTCGGTTCCCAGGTTGGAAGATTATCTCACCCGGCCCCAGCTATATA
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                   2007 GGCCCAGCAGGCCCAACTCCAGGGATTCCTTCCACGACAGAAAACATACAAGACTCCTT
                                               182 GGCCCAGCAGCAACTCCCAGGATTCCTTCCACGACAAAAACATACAAGACTTCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; foam cell differentiation; atherosclerosis; cerebral stroke; cardiovascular disorder; coronary artery disease; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                              Human DNA sequence #158 expressed during foam cell differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 144.4; DB 24; Length 1889; Pred. No. 8.9e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seilhamer JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              α,
                                                                                                                                                                                                                                                                                     BP.
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                                                                                                                                                                                                                                                                                     AAS94903 standard; DNA; 1889
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                                                                                                                                                                                                                                                                                                                                                                                    14-FEB-2002 (first entry)
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Matches 145; Conservative
                                                                                                                  CAGCCAAC 2074
                                                                                                                                                               242 CAGCCAAC 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The patent discloses novel target genes abnormally expressed in heart tissues and their corresponding proteins. The invention also relates to methode for assessing the expression level of these genes. The method is used for testing the predisposition of mammals and preferably humans for a heart disease or for an acute state of such a disease. It is also useful to treat diseases of the heart such as congestive heart failure, dilative cardiomyopathy, hypertrophic cardiomyopathy, ischaemic cardiomyopathy, specific heart muscle disease, rhythm and conduction disorders, syncope and sudden death, coronary heart disease, systemic arterial cardiomary phypartension, pulmonary heart disease, systemic arterial heart disease, pericardial disease, valvular heart disease, congenital heart disease, pericardial disease and endocarditis. Sequences of the invention are also used in gene therapy.

A transgenic non-human mammal comprising the sequences of the invention are useful for the development for medicaments for the treatments of heart diseases. The present DNA sequence is expressed sequence tag (EST) clone X83703 which encodes CAAS8676 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying a subject at risk for a heart disease e.g. congestive heart failure, dilative cardiomyopathy, heart muscle disease, by quantifying the polypeptide expressed by genes abnormally expressed in heart tissue
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Pred. No. 2.8e-43;
0; Mismatches 5; Indels 1;
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                                                                                                                                                                                                                                                                 '*tag= b
'note= "AU-rich mRNA decay element"
                                                                                                                                                                                                                                                                                                                                                             'note= "AU-rich mRNA decay element"
                                                                                                                                                                                        /*tag= b
'note= "AU-rich mRNA decay element"
product= "Human CAA58676 protein"
                                                                                                                     '*tag= b
'note= "SIMC01-1 cDNA fragment"
                   198..431
/*tag= b
/note= "66268 cDNA fragment"
1604..1753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 97.6%;
Matches 242; Conservative
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P-PSDB; AAE16633.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes a combination of cDNAs (designated BC-CDNAs), which are differentially expressed in breast cancer. The combination includes 152 cDNA sequences, or their complements. The protein encoded by any of these BC-CDNAs is useful for screening several molecules or compounds to identify at least one ligand that specifically binds the protein, producing or preparing polyclonal or monoclonal antibodies, or purifying antibodies from a sample. The antibodies, which specifically bind the protein differentially expressed in breast cancer is useful for detecting the expression of a protein in a sample. The BC-CDNAs are also useful for diagnosing, monitoring the treatment of, or staging, breast cancer. This sequence represents a differentially expressed breast cancer associated cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 GAGGGAGTGTTACTTCGGTTCCCAGGTTGAAAGATTATCTCACCCGGCCCCAGCTATATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form part of the ed specification, but was obtained in electronic format directly the US patent office at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            breast
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                                                                                                                                                                                                                                                                                                                                                                                                                                        New cDNAs, which are differentially expressed in (metastatic) t
cancer useful for diagnosing or staging, breast cancer, or for
monitoring the treatment of breast cancer in an individual
                                                                                                                                                                   Differentially expressed breast cancer associated cDNA #143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.0%; Score 144.4; DB 25; Length 1
99.3%; Pred. No. 8.9e-24;
Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                      88.
                                                                                                                                                                                          Breast cancer; differential gene expression; BC-cDNA; breast cancer diagnosis; breast cancer monitoring; breast cancer staging; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1889 BP; 613 A; 354 C; 452 G; 469 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      segdata.uspto.gov/seguence.html?DocID=20020156263.
        2049 AAACATACAAGACTCCTTCAGCCAAC 2074
                      125 AAACATACAAGACTCCTTCAGCCAAC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 182; 30pp; English.
                                                                                             BP.
                                                                                           ABX77648 standard; cDNA; 1889
                                                                                                                                                                                                                                                                                                                                           05-OCT-2000; 2000US-238331P.
                                                                                                                                                                                                                                                                                                                  04-OCT-2001; 2001US-0974298
                                                                                                                                            (first entry)
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Best Local Similarity
                                                                                                                                                                                                                                                                  US2002156263-A1.
                                                                                                                                                                                                                                                                                                                                                                   (CHEN/) CHEN H.
                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                         09-APR-2003
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20646 AATAACTAAGCACGGTGCTCGCTTCGGCAGCACATATACTAAAATTGGAACGATACAGAG 20705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:68.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human 1p36 homozygosity deletion domain from the 36-position of first chromosome short arm in human neuroblastoma cell lines, applicable e.g. in gene diagnosis of tumors as well as in developing anti-cancer drugs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anticancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; chromosome 1; 1p36; neuroblastoma cell line; NB-1; anticance, tumour suppressor; human 1p36 homozygosity deletion domain; tumour; diagnosis; ds.
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Pred. No. 2.4e-12;
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2049 AAACATACAAGACTCCTTCAGCCAAC 2074
                                           AAACATACAAGACTCCTTCAGCCAAC
                                                                                                                                                                                                                                                               AAF97854 standard; DNA; 34488 BP.
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09-MAY-2000; 2000JP-0136266.
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Matches 123; Conservative
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RESULT 10

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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                              Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23092.
                                                                                                               cytostatic; gene therapy; vaccine; metastasis; ds.
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2000US-0229287.
2000US-0229343.
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2000US-0225267
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2000US-0226279
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2000US-0227182
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2000US-0232400
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                                 06-NOV-2001 (first entry)
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14-AUG-2000;
14-AUG-2000;
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                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-AUG-2000;
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14-AUG-2000;
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                                                                                                                                                                                                               09-AUG-2001
AAK68280;
   47492 AATAACTAAGCACGGTGCTCGCTTCGGCAGCACATATACTAAATTGGAACGATACAGAG 47551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47552 AAGATTAGCATGGCCCCTGCGCAAGGATGACACGCAAATTCGTGAAGCGTTCCATATTTA 47611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes the coding and protein sequences of the human kinesin-like protein HKLP. It is thought that the protein could be involved in neurological disorders, infertility, spontaneous abortion, neonatal chromosome disorders, aneuploidy and cancers. This is due to its function in the movement of microtubules. The protein shows homology to the murine KIFLA and KIFLB proteins. The sequences disclosed in the invention can be used in the isolation of similar human proteins and in vector production. In addition, the biallelic markers shown can be used in disease diagnosis and population studies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 AAATAGTAATGACTCTGTTTGCTTCAGCAGGACATATACTAAAATAGGAGCTATACAAAG 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318 AAGATTAGCATGGACTCTGTGCAAGAATGACACACAAATTTGTGAAACATTCCATATATT 377
                                                                                                                                                                                                             Human; kinesin-like protein; HKLP; KIF1; cell division; cancer;
intracellular transport; neurological disorder; infertility;
biallelic marker; spontaneous abortion; neonatal chromosome disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       An isolated or purified human kinesin-like protein (HKLP) encoding polynucleotide used to detect HKLP polynucleotides in a sample comprises a contiguous span of at least 12\ \mathrm{nucleotides}.
                                                                                                                                                                               Human kinesin-like protein HKLP coding sequence contig SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 121162 BP; 33272 A; 24108 C; 25842 G; 37919 T; 21 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.7%; Score 97.2; DB 21; Length 121162; 14.1%; Pred. No. 3.6e-12; [ve 0; Mismatches 43; Indels 0; 0]
 378 AAAAATAAATAAATAAAGAGAAAAGGAAAAATTAAAAAGAAA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grel P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 143-175; 199pp; English
                                                                                  AAC66548 standard; DNA; 121162 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bougueleret L, Dufaure-Gare I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAK68280 standard; DNA; 7141 BP
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                                                                                                                                                 19-FEB-2001 (first entry)
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Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-665242/64.
                                                                                                                                                                                                                                                                                                                               WO200063375-A1
                                                                                                                                                                                                                                                              aneuploidy; ds
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                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                  AAC66548;
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RESULT 11

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AAK68280 ID AAK6 XX

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05-DEC-2000;
06-DEC-2000;
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                                                                                                                                         17-NOV-2000
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's sgenome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
cs supplement the patients own production of (I). Additionally, (I)
cc polynucleotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
cc cancers and cancer metastases of haematopoietic-derived cells. AAK64703
cc cancers and cancer metastases of haematopoietic antigen genomic
concers and cancer metastases of haematopoietic antigen genomic
sequences from the present invention. AAK84942 to AAK84950 and AAM82169
crepresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1136 AIATATAGTATTTGTGGTAGAGATGGGATTTTGCCATGTTGCCCAGGCTAGTATTGAACT 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCACTGCACCGGCTGATAGCTGGTTTCATTTACTCTATTTCTTGACCACTCTGATCCAT 1314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3982 CCACCACACCTGGCCGTGAACT-TTTTCTTTCCCTTTATTTTCAAAAAAGAATGTTTCAT 4040
                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3862 ATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTGCCCAGGCTAGTTTTGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1196 CCTAAGCT-AAGCAATCTTCCTGTCTCTGCCTCCCAAAATGTTGGGATTACAGGTGTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3922 cereagerecagecantergecraceregecreecaaangeragarracagargraag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomic sequence #435 encoding for novel human respiratory antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 23092; 3071pp + Sequence Listing; English.
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4.6%; Score 95.6; DB 22; Length 7141;
Best Local Similarity 70.3%; Pred. No. 3.3e-12;
Matches 156; Conservative 0; Mismatches 64; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7141 BP; 2053 A; 1477 C; 1612 G; 1999 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1315 TTTGAAGTAAAATGCTCCAATTATTATGCTGTTTTAGAACA 1356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4041 CATCCATTTTTGTGATTAGATTATGGTTATATTATATA 4082
                                                                                                                                                                                                                                                     Ruben SM;
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AAS28595 standard; DNA; 6040 BP.
                  08-DEC-2000; 2000US-0251868.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251999.
08-DEC-2000; 2000US-0251999.
11-DEC-2000; 2000US-025990.
05-JAN-2001; 2001US-0259678.
                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
  2000US-0251856
                                                                                                                                                                                                                                                     Barash SC,
                                                                                                                                                                                                                                                                                                    WPI; 2001-483426/52
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                                                                                                                                                                                                                                                                                                                                                                                                         metastasis
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25-SEP-2000; 2000US-0234999.
26-SEP-2000; 2000US-0234998.
27-SEP-2000; 2000US-0234998.
27-SEP-2000; 2000US-0238344.
29-SEP-2000; 2000US-0238334.
29-SEP-2000; 2000US-0238337.
29-SEP-2000; 2000US-0238337.
29-SEP-2000; 2000US-0238337.
29-SEP-2000; 2000US-0238337.
29-SEP-2000; 2000US-0238337.
29-SEP-2000; 2000US-023833937.
20-OCT-2000; 2000US-023833937.
20-OCT-2000; 2000US-02383937.
20-OCT-2000; 2000US-02341809.
20-OCT-2000; 2000US-02441809.
20-OCT-2000; 2000US-0244210.
20-OCT-2000; 2000US-0244211.
20-OCT-2000; 2000US-0244211.
20-OCT-2000; 2000US-0244211.
20-OCT-2000; 2000US-0244211.
20-OCT-2000; 2000US-0244211.
20-OCT-2000; 2000US-0244211.
20-OCT-2000; 2000US-0244221.
20-OCT-2000; 2000US-0244221.
20-OCT-2000; 2000US-0244221.
20-OCT-2000; 2000US-024221.
20-OCT-2000; 2000US-024221.
20-OCT-2000; 2000US-024221.
20-OCT-2000; 2000US-024222.
20-OCT-2000; 2000US-02422.
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08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
      anti allergic, anti asthmatic; anti inflammatory; olfactory; respiratory active; ds.
                                                                                                                                       17-JAN-2001; 2001WO-US01333
                                                                            WO200155448-A1
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05-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
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08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
12-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
                                                 Homo sapiens.
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14-AUG-2000;
14-AUG-2000;
21-AUG-2000;
22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
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01-SEP-2000;
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19-MAY - 2000; 20000S-020515.

07-JUN-2000; 2000US-0219467.

20-JUN-2000; 2000US-0214886.

30-JUL-2000; 2000US-021687.

07-JUL-2000; 2000US-0216880.

11-JUL-2000; 2000US-0216880.

11-JUL-2000; 2000US-021689.

14-JUL-2000; 2000US-021890.

26-JUL-2000; 2000US-021890.

26-JUL-2000; 2000US-021890.
                                                                                                                                                                                     26-JUL-2000; 2000US-0220964.
14-AUG-2000; 2000US-0224518.
14-AUG-2000; 2000US-0224519.
14-AUG-2000; 2000US-0225213.
14-AUG-2000; 2000US-0225264.
14-AUG-2000; 2000US-0225266.
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14-AUG-2000; 2000US-0225447
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18-AUG-2000; 2000US-0226279
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22-AUG-2000; 2000US-0226868
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01-SEP-2000; 2000US-0229343
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2000US-0232081
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  The present invention relates to the isolation of novel human respiratory antigens (AAU17885-AAU17955), and cDNA and genomic sequences encoding for these polypeptides. The sequences of the invention are useful for preventing, treating and/or prognosing disorders ledge. vocal cord paralysis, tonsilitis, and laryngitis), ung disorders e.g. pneumonia, allergic disorders e.g. asthma, pleurisy, cystic fibrosis, emphysema, nose disorders and cancers of the invention are useful in gene therapy and antisense therapy. AAS28161-AAS28764 represent genomic sequences encoding for novel the invention are useful in gene therapy and antisense therapy. AAS28161-AAS28764 represent genomic sequences encoding for novel Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39455.
                                                                                                     Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the respiratory system including respiratory cancers and also for testing and detection e.g. diagnosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACTGCACCCGGCTGATAGCTGGTTTCATTTACTCTATTTCTTGACCAC 1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.6%; Score 95.4; DB 22; Length 6040; 72.8%; Pred. No. 3.5e-12; tive 0; Mismatches 46; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6040 BP; 1446 A; 1488 C; 1420 G; 1686 T; 0 other;
                                                                                                                                                            Disclosure; SED ID No 1029; 546pp; English
                                                   Ruben SM
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ID AAK84643 standard; DNA; 4181 BP.
                         (HUMA-) HUMAN GENOME SCI INC.
05-JAN-2001; 2001US-0259678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000; 2000US-0180628.
24-FEB-2000; 2000US-0184664.
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                                                                                                                                                                                                                                                                                                                                                                                                                              4.69
Best Local Similarity 72.89
Matches 123, Conservative
                                                   Rosen CA, Barash SC,
                                                                              WPI; 2001-476224/51
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cativity, and can be used in AMM81210 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (1) proteins and polymucleotides may be used in the prevention diagnosis and treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expression in a patient's genome cupplement the patients own production of (1). Additionally, (1) polymucleotides may be used to produce the secreted (1), by inserting polymucleotides may be used to produce the secreted (1), by inserting protein. (1) proteins and polymucleotides may be used to produce the secreted (1), by inserting protein. (1) proteins and polymucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK49421 to AAK84960 and AAM82169 represent sequences used in the exemplification of the present invention.
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4.5%; Score 94; DB 22; Length 4181;
Best Local Similarity 58.9%; Pred. No. 6.6e-12;
Matches 178; Conservative 1; Mismatches 122; Indels 1
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04-FEB-2000; 2000US-0180628.
24-FEB-2000; 2000US-0184664.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 39455; 3071pp + Sequence Listing; English
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02-OCT-2000; 2000US-0237040.

13-OCT-2000; 2000US-023935.

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08-NOV-2000; 2000US-0246476.

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17-NOV-2000; 2000US-024921.

17-NOS-2000; 200U 2000US-0251030 2000US-0251988 2000US-0251988 2000US-0251479 2000US-0251866 2000US-0251868 2000US-0251989 2000US-0251990 06-DEC-2000; 08-DEC-2000; 08-DEC-2000; 08-DEC-2000; 

SM; Ruben (HUMA-) HUMAN GENOME SCI INC Barash SC, G, Rosen

human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and Nucleic acids encoding luseful for preventing, metastasis -WPI; 2001-483426/52

+ Sequence Listing; English Disclosure; SEQ ID NO 23094; 3071pp

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2000US-0227182
                                                                    2000US-0220963
2000US-0220964
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    AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient segment contracts of the affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK84950 and AAM82169 represent invention.
                                                                                                                                                                                                                                                                                                                             1136 ATATATAGTATTTGTGGTAGAGATGGGATTTTGCCATGTTGCCCAGGCTAGTATTGAACT 1195
                                                                                                                                                                                                                                                                                                                                                                                  1196 CCTAAGCT-AAGCAATCTTCCTGTCTCTGCCTCCCAAAATGTTGGGATTACAGGTGTAAG 1254
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                                                                                                                                                                                                                                                                                                                                                       3862 ATTTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTGCCCCAGGCTAGTTTTTGAACT 3921
                                                                                                                                                                                                                                                                                                                                                                                                          3922 ccrgagcrcaggcarcrgccraccrcggcrcccaaargcraggarracaggrgrgag 3981
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cytostatic; gene therapy; vaccine; metastasis; ds.
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4.5%; Score 94; DB 22; Length 7141;
Best Local Similarity 69.8%; Pred. No. 7.9e-12;
Matches 155; Conservative 0; Mismatches 65; Indels 7.
                                                                                                                                                                                                                                               Sequence 7141 BP; 2053 A; 1476 C; 1615 G; 1997 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1315 TTTGAAGTAAAATGCTCCAATTATTATGCTGTTTTAGAACA 1356
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2000US-0214886.
2000US-0215135.
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2000US-0184664
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2000US-0198123
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PR 20-CCT-2000; 200008-2011806. PR 20-CCT-2000; 200008-2011806. PR 20-CCT-2000; 200008-2011806. PR 20-CCT-2000; 200008-2011826. PR 20-CCT-20009-20008-2011826. PR 20-CCT-20009-20008-2011826.
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51170 TAATTTTGTATTTTGGTAAGATGGGGTTTCACCATTTTGGCCAGGCTGGTCTTGAAT 51111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCTAAGCTAAGCAATCTTCCTGTCTCTCCCCAAAATGTTGGGATTACAGGTGTAAG 1254
supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invontion. AAK5492 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCTGACCCAAGTGATCTCCCTGCCTCTCCCAAAGTGCTGGGATTACAGGTGTGAA
                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                     Query Match
4.5%; Score 93.6; DB 22; Length 52845;
Best Local Similarity 67.3%; Pred. No. 1.9e-11;
Matches 132; Conservative 0; Mismatches 64; Indels. 0;
                                                                                                                                                                                                                                                                    Sequence 52845 BP; 14698 A; 11081 C; 10505 G; 16561 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                    64; Indels.
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AracB polylinker. Plasmid pUP1-1 con Primer for amplyfy Primer B for mouse

AAZ39184

polylinker D

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AAC87604 AAD44897 AAD44911 AAD44914

ABK89689

ABK71151 AAL45762

ABK68247 AAQ85550 AAL45719

Capture DNA oligom Circular plasmid e Oligonucleotide 40 Plasmid p182Sfil c M13mp18 single-str

> AAT88401 AAT46199 AAX88900 ABA98175

AAQ96167 AAT47083 ABL51437

Stabiliser sequenc

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"bases 1-10 are derived from the ROR2 gene"
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|/*tag= b
|/note= "bases 11-45 are derived from Bluescript
| polylinker"
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/note= "LacZ coding region initiation codon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Orphan receptor; ROR2; mouse; cartilage; chondrocyte; osteoarthritis; therapy; mutant; beta-galactosidase; LacZ;
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AAH26804;
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Plasmid araCB poly
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     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                      nucleic search, using sw model
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AAZ50271
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ALIGNMENTS

BP.

used to produce transgenic

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the BAC end region in potato genomic DNA. The BAC sequences are used to inhe back end region in potato genomic DNA. The BAC sequences are used to identify the potato Rx gene. The Rx gene (AAZ37153) is a resistance gene which confers extreme resistance against potato virus X (PVX).

Sequence AAZ37154 is the Rx coding sequence free from introns. The Rx cesistance polypeptide AAY52152, this vector which encodes the Rx resistance polypeptide AAX5125. This vector can be used to transform plant cells to produce a transgenic plant with resistance to PVX. The Rx gene can be used to engineer resistance traits, preferably broad spectrum carrame resistance, into plants. The Rx gene can also be activated by non-PVX viruses, e.g. Narcissus mosaic virus (NMV), Nandina virus X (NVX), viola mosaic virus (WMV), Cymbidium mosaic virus (WAMV), Poplar mosaic virus (POpMV) and White clover mosaic virus (WCIMV). Rx can be used to offer specific protection against this group. The Rx gene can be used to create antibodies specific for Rx. The antibodies can be used to create antibodies specific for the detection, identification or isolation of Rx or homologues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Resistance gene; Gpa2; potato; phytopathogenic nematode; chromosome 12p; marker; IPM4c; 111R; Potato Cyst Nematode; PCN; Globodera; nematicide; nucleotide binding site; NBS; nematode resistance; detection; diagnosis; PCR primer; BAC clone; potato DNA insert; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer AB3 to amplify right end sequence of the potato DNA insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.9%; Score 21; DB 20; Length 22; 100.0%; Pred. No. 14; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22 BP; 5 A; 7 C; 6 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated plant virus resistance gene, plants with resistance to virus infection
                                                                                                                                                                                                                                                                                                              Kanyuka KV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 71; 124pp; English.
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                                                                                                                                                                                                                                                                                                              Baulcombe DC,
                                                                                                                                                                                                                                                         (PLAN-) PLANT BIOSCIENCE LTD
                                                                                                                                          99WO-GB01182
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                                                                                                                                                                                                                                                                                                                 Bendahmane A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of the fusion region between a mouse ROR2 gene (see also AAH26803) and the polylinker region of Bluescript plasmid, which is flanked by a beta-aglactosidase Lac2) coding region. Disruption of the endogenous murine ROR2 allele by insertion into Bluescript resulted in a sequence concoding a novel product (see AAB82917) in which the ecto- and transmembrane domains of ROR2 were fused to Lac2, which replaced to mormal tyrosine Kinase-like cytodomain. This provided for simultaneous knocking out of ROR2 function and the capability of Lac2 staining to follow ROR2 expression patterns. Mice heterozygous for the mutant allele (ROR2+/-) were viable, fertile and appeared normal. ROR2 was selectively expressed in the chondrocytes of the ceveloping anlagen of all bones formed by endochonical ossification. Mice homozygous for the ROR2 mutant allele (ROR2-/-) exhibited perinatal lethality, with shortened snout, limbs and tail as well cas cleft palate. Thus, disruption of the mutine ROR2 gene leads to profound skeletal abnormalities. As ROR2 appears to play a critical role in cartilage formation it may be useful in developing strategies to treat diseases of cartilage such as solved the real planks of the mutant all the real place of the mutant all the real
                                                                                                                                                                                                                                                                                                                                                                      Increasing chondrocyte growth, development and activity, for increasing cartilage formation, comprises contacting chondrocytes expressing orphan receptor ROR2 with an agent capable of activating ROR2 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 2.1e-05;
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100.0%; Pred. No. 2...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1; 31pp; English
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                                                                                                         14-MAR-2000; 2000US-189216P
                                                                                                                                                                       (REGE-) REGENERON PHARM INC
                                                                                                                                                                                                                            De Chiara TM, Kimble R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 33; Conservat
                                                                                                                                                                                                                                                                                    WPI; 2001-590052/66.
P-PSDB; AAB82917.
20-SEP-2001
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receptor.

Query Match Matches

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Gaps

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99WO-NL00491. 98WO-NL00445

30-JUL-1999;

31-JUL-1998;

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WPI; 2000-195310/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present DNA sequence is the PCR primer AB3, used to amplify the right end sequence of the potato DNA insert in the BAC clone. The recircularised BAC clone with the potato DNA insert is used as the template for the amplification. This primer is used to screen Cara BAC inbrary with markers IPM3, IPM4 and IPM5 and to isolate BAC clones from the RA1/Gpa2 locus. The Gpa2 gene confers resistance to infections by phytopathogenic nematode of the Globodera genus. It is mapped to short arm of chromosome 12 (12p), between the markers IPM4c and 11R. This arm of chromosome 12 (12p), between the parkers IPM4c and 11R. This coup is associated with resistance to Potato Cyst Nematodes (PCN) like G. pallida and G. rostochiensis, that invade and damage the roots of Solanaceae. It has nematocidal activity. A recombinant DNA sequence Comprising the Gpa2 gene sequence can be transformed or transfected into plants, to provide increased resistance to nematodes. The polypeptides of comprising the used in nematicide compositions and for detection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                          producing plants which are resistant to nematodes and polypeptides for use in nematicide compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Resistance; Gpa2; potato; phytopathogenic nematode; chromosome 12p; marker; IPM4c; 111R; Potato Cyst Nematode; PCN; Globodera; nematicide; nematode resistance; detection; diagnosis; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                  Bakker J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bakker J;
                                                                                                             New isolated Gpa2 nematode resistance gene from potato, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer AB3 to amplify right end sequence of the potato DNA insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                  Lankhorst RMK,
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lankhorst RMK,
                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
             CPRO-DLO CENT PLANTENVEREDELINGS REPROD. LANDBOUWUNIVERSITEIT WAGENINGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                  ch 0.9%; Score 21; DB 21; 1 Similarity 100.0%; Pred. No. 14; 21; Conservative 0; Mismatches 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CPRO-) CPRO-DLO CENT PLANTENVEREDELINGS REPROD. (UYWA-) LANDBOUWUNIVERSITEIT WAGENINGEN.
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22 BP; 5 A; 7 C; 6 G; 4 T; 0 other;
                                                  Van Der Vossen EAG, Van Der Voort JNAMR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Van Der Voort JNAMR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2325 AGCITGCATGCCTGCAGGTCG 2345
                                                                                                                                                                Example 3; Page 26; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                    diagnosis of nematode infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 AGCTTGCATGCCTGCAGGTCG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-NL00445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ50660 standard; DNA; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAY-2000 (first entry)
                                                                                     WPI; 2000-183132/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Van Der Vossen EAG,
                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Solanum tuberosum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200006753-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stiekema WJ;
                                                               Stiekema WJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA250660;
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
              (CPRO-)
                        UYWA-)
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The present sequence is the PCR primer AB3, used to amplify the right end sequence of the potato DNA insert in the BAC clone. The recircularised BAC clone with potato DNA insert is used as template for the amplification. This primer is used to screen Cara BAC library with markers IPM3, IPM4 and IPM5 and to isolate BAC clones from the RA1/Gpa2 locus. Gpa2 gene confers resistance to infection by phytopathogenic nematode of the Globodera genus. It is mapped to short or chromosome 12 (12p), between the markers IPM4c and 111R. This arm of chromosome 12 (12p), between the markers IPM4c and 111R. This local or chromosome is associated with resistance to Potatoc Cyst Nematodes (PCN) like G. pallida and G. rostochiensis, that invade and damage the roots of Solanaceae. It has nematocidal activity. Recombinant DNA sequence compassing gene can used to produce transgenic plants with increased resistance to nematodes. The polypeptides can also be used in nematicide compositions and for detection and diagnosis of nematode
Recombinant Gpa2 polynucleotide from potato, Solanum tuberosum, useful to confer resistance to phytopathic nematodes of the genus Globodera in transgenic plants, e.g. resistance to potato cyst nematodes in potatoes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rapamycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rapamycin; neomycin resistance; antifungal; anticancer; neurotrophin; immunosuppressant; polyketide synthase; cytostatic; neurotrophic; antitumour; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant Streptomyces hygroscopicus, for producing new compounds, useful as e.g. anticancer agents, contains altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 21; DB 21; Length 22;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 22 BP; 5 A; 7 C; 6 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Pred. No. 14;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neomycin cassette related PCR primer #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2325 AGCTTGCATGCCTGCAGGTCG 2345
                                                                                                                                                                                     Example 3; Page 26; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page 50; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 AGCTTGCATGCCTGCAGGTCG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH41892 standard; DNA; 24 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KOSA-) KOSAN BIOSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.9%;
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20-APR-2000; 2000US-0198578.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces hygroscopicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu L, Chung LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-355490/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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AAH41892/c
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present invention describes a recombinant Streptomyces hygroscopicus
       (A) that produces rapamyoin compounds (1). Also described are: expressee a hybrid PKS (polyketide synthase) comprising at least part of each of rapamyoin PKS and heterologous PKS; (3) recombinant S. hygroscopicus that does not express at least one rapamyoin modifying enzyme but does produce a rapamyoin analogue; and (4) recombinant S. hygroscopicus that expresses a PKS consisting of only part of a rapamyoin PKS. (A) has cytostatic, antifungal, immunosuppressant and neurotrophic activities. (I) are useful as antitumour, antifungal or immunosuppressant agents and neurotrophics, and also as intermediates for other active compounds. Modular construction of PKS makes possible production of a large number of hybrids for screening. The present sequence represents a PCR primer which is used in an example from the
                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proline-rich extensin-like receptor kinase; PERK; resistance;
                                                                                                                                                                                                                         Score 21; DB 22; Length 24;
Pred. No. 14;
                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                 0.9%; Sco.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                 Sequence 24 BP; 5 A; 7 C; 7 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                            AGCTTGCATGCCTGCAGGTCG 2345
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                                                                                                                                                                                                                                                                                                                                                                 ВР
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99US-0159122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-AUG-2000; 2000WO-CA00966
                                                                                                                                                                                                                                                                                                                                                                AAF77092 standard; DNA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         PERK1 cloning primer #1.
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                                                                                                                                                                                                                                     Local Similarity
ses 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GORING D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GORI/) GORING D (SILV/) SILVA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brassica napus.
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13-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plant; ds
                                                                                                                                                                                                                                                                                                                                                                                         AAF77092;
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                                                                                                                                                                                                                          Query Match
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New proline-rich, extensin-like receptor kinase nucleic acids and polypeptides useful for increasing plant wounding or pathogen resistance, or for producing transgenic plants with increased wounding

Examples; Page 45; 91pp; English.

or pathogen resistance

The present invention relates to proline-rich extensin-like receptor kinase (PERK). The PERK nucleic acids and polypeptides are useful for increasing the resistance of plants to wounding and pathogens. These are also useful for producing transgenic plants with increased wounding and pathogen resistance compared with a wild type plant, as well as in assays for identifying and developing compounds to inhibit and/or enhance polypeptide

function directly

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rheumatoid arthritis, where overexpression of the protein can damage the extracellular matrix. Chitinase also improves the activity of other antifungal agents and may allow a reduction in the dose of such agents,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV10441-V10443 are primers used to amplify the Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 Chitinase, human, fungal infection, immunogen, diagnosis, treatment, Gaucher's disease, transgenic, detection, hybridisation, antifungal, rheumatoid arthritis, overexpression, extracellular matrix, arabinose, promoter, BAD operon, arac gene, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding human chitinase - useful as antifungal agents, especially in combination with other antifungals
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                                                   Length 27;
                                                                                       Indels
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                                                 DB 22;
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               Sequence 27 BP; 6 A; 7 C; 9 G; 5 T; 0 other;
                                                                Local Similarity 100.0%; Pred. No. 14 les 21; Conservative 0; Mismatches
                                                   0.9%; Score 21;
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                                                                                                                           2325 AGCTTGCATGCCTGCAGGTCG 2345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 15; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                  Plasmid araCB polylinker region.
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Matches 21; Conservative 0;
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                                                                                                                                                                                                                                                          ВР
                                                                                                                                                                                                                                     AAV10443/c
ID AAV10443 standard; cDNA; 30
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                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                          AAV10443;
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                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gray PW;
                                                                      Best Loca
Matches
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AGCTTGCATGCCTGCAGGTCG 9

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The present sequence is the polylinker region of plasmid araBC contains the araC gene promoter, which was isolated from the arabinose operon BAD of Salmonella typhimurium. It was used to express human A-kinase anchor protein 79 (ARAP 79). By binding both cAMB-dependent protein kinase (PKA) and calcineurin, AKAP 79 co-localises a kinase and a protein kinase (PKA) and calcineurin, AKAP 79 co-localises a kinase and a phosphatase that may regulate flux through a specific signalling pathway. Calcineurin is a Ca2+/calmodulin-dependent protein phosphatase which is involved in many intracellular signalling pathways. It participates in regulation of IL-2 expression following T cell stimulation in T cells. Calcineurin-binding peptides derived from AKAP 79 may be used to inhibit calcineurin-binding peptides derived from AKAP 79 may be used to inhibit calcineurin activity in a cell. The peptides are useful for treating T cell-mediated disorders. Calcineurin deletion mutants which bind AKAP 79 are useful for defining an AKAP 79 binding site, for stimulating expansion, or for enhancing T cell responses to experimental stimule for evaluation of early events in T cell biology and activation of the immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel calcineurin deletion mutant having calcineurin polypeptide sequence and binding A-kinase anchor proteins, for treating graft rejection following organ transplantation and T cell-mediated disorders
                                                                                                                                                            A-kinase anchor protein, AKAP, AKAP 79; immunostimulant;
interleukin 2 expression modulation; graft rejection; transplantation;
                                                                                                                                           araCB; arabinose operon; BAD; araC gene; calcineurin-binding peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
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100.0%; Pred. No. 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Howard ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 30 BP; 7 A; 8 C; 8 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 14;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 13; Column 23-24; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.08; Pic
                                                                                                        Plasmid araCB polylinker region.
                                                                                                                                                                                                    cell-mediated disorder; ds.
                                                                                                                                                                                                                                                                                                                                                                                   94US-0344227.
95US-0404731.
95US-0503226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallatin WM,
                                                                                                                                                                                                                                                                                                                                                  96US-0721458
AAA94281 standard; DNA; 30
                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-578541/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ICOS-) ICOS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lockerbie RO,
                                                                                                                                                                                                                                                                                                                                                 27-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                     23-NOV-1994;
                                                                    08-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                         17-JUL-1995;
                                                                                                                                                                                                                                                                          US6107104-A.
                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Matches
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The invention relates to chitinase derived polypeptide, chitin-binding fragments of human chitinase, fragment analogues, purified and isolated polymuclectides encoding such fragments. The invention is used for treating fungal infections and for detecting and binding chitin. The present sequence is a araCB polylinker DNA used in the exemplification
                                                                                                                                                                                                                                                                                                                                   chitinase derived polypeptides used for treating fungal infections for detecting and binding chitin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                Chitinase; chitin-binding fragment; therapy; fungal infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.9%; Score 21; DB 24; Length 30; 100.0%; Pred. No. 14; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chitinase; enzyme; fungicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 30 BP; 7 A; 8 C; 8 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                    Example 3; Column 43; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2325 AGCTTGCATGCCTGCAGGTCG 2345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 AGCTTGCATGCCTGCAGGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL57388 standard; DNA; 30 BP.
RESULT 9
AAD42624/c
ID AAD42624 standard; DNA; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0877599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabinose; promoter; araC; antifungal; infection; ss.
                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella typhimurium.
                                                                                                                                                                                                                                                                                       Gray PW, Tjoelker LW;
                                                                                          AraCB polylinker DNA
                                                                                                                                                                                                                                                                                                              WPI; 2002-606631/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
es 21; Conserv
                                                                                                                                                                                                                                                                (ICOS-) ICOS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AraCB polylinker.
                                                                                                                                                Unidentified
                                                                                                                                                                                                                    12-MAR-1999;
                                                                                                                                                                                                                                           12-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6372212-B1
                                                                  15-NOV-2002
                                                                                                                                                                                               04-JUN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-APR-2002
                                                                                                                            fungicide;
                                             AAD42624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches
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2325 AGCTTGCATGCCTGCAGGTCG 2345

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AGCTTGCATGCCTGCAGGTCG

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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccine, delivery, hyperblebbing strain; Neisseria gonorrheae, bleb; blebosome, antigen, diagnosis, immunisation; immunostimulant, viral disease; rabies; hepatitis; bacterial disease; salmonella; pneumonia; fungal disease; parasitic disease; infection; ss.
                                                                                                                                                                                                                                                                                                             The present sequence is that of an araCB polylinker flanked by a 5. XbaI site and a 3. HindIII site. The polylinker was used in the construction of expression plasmid paraMo218, in which human chitinase cDNA (see ABL57380) was under the control of the Salmonella arabinose promoter. The plasmid was used to transform Escherichia coli cells for recombinant production of a chitinase analogue (see ABB76294). The invention provides human chitinase polynucleotides and polypeptides, and methods for the recombinant production of human chitinase products, for use in treating fungal infections. Human chitinase can be used to improve the activity of a non-chitinase antifungal agent in the treatment of candidiasis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aspergillosis, coccidioidomycosis, blastomycosis, paracoccidioidomycosis, histoplasmosis, cryptococcosis, cryptococcosis, chromoblastomycosis, sporotrichosis, mucormycosis, dermatophytoses
                                                                                                                                                                               Co-administering chitinase to improve the effectiveness of fungici drugs e.g. amphotericin B or itraconazole, useful for treating fun infections e.g. candidiasis, coccidioidomycosis and blastomycosis
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel vaccine for providing immunity against disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.9%; Score 21; DB 24;
100.0%; Pred. No. 14;
1ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 30 BP; 7 A; 8 C; 8 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                       Example 3; Column 10; 26pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYMA-) UNIV MARYLAND BALTIMORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ilarity 100.0%; P. Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Pneumocystis infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0081576.
96US-0663618
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                                                                                                                                     WPI; 2002-442449/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 21; Conserv
                                              (ICOS-) ICOS CORP.
    14-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ39184;
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                                                                                           Gray PW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ39184/C
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The present invention describes a vaccine for providing immunity against a disease. The vaccine comprises blebosomes where an immunogenic polypeptide specific for the disease is present in a pharmacologically effective dose in a pharmaceutically acceptable excipient. The vaccine is useful in the form of a pharmaceutical composition for treating a disease, comprising a blebosome where the polypeptide (especially a cytokine, a receptor and/or an antibiotic) is active against the disease. Immunisation against diseases and are useful in diagnostic assays where the presence of antibodies against disease can be detected in samples from a patient suspected of having the disease can be detected in samples viral diseases such as rabhes or hepatitis, bacterial diseases such as almonella or pneumonia, fungal diseases and parasitic diseases. The blebosomes are also useful in a delivery system for other biological molecules, e.g. chemotherapeutic agents for use in chemotherapy or immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antigens are present in the absence of other cellular components. In addition the antigens are assembled in a natural biological membrane allowing the antigen to form a native conformation more closely minicking what is encountered in the natural organism. The present sequence represents an oligonucleotide used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enhancers/suppressors. Vaccines using blebosomes collected from hyperblebbing strains have an advantage over conventional vaccines as the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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antigen-mediated and antigen-initiated diseases, such as toxic shock
syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Toxic shock syndrome; toxin; TSST-1; Staphylococcus aureus; superantigen; mutant; derivative; deletion; substitution; vaccine; treatment; prophylactive; antibody response; T-cell; thymocyte; MHC; major histocompatibility complex; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer for amplyfying S. aureus toxic shock syndrome toxin gene.
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100.0%; Pred. No. 14;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 32 BP; 7 A; 8 C; 10 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kappler JW, Marrack P, Matsumura M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2325 AGCTTGCATGCCTGCAGGTCG 2345
Example 1; Page 26; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 AGCTTGCATGCCTGCAGGTCG 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-259474/26
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Gaps

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improve——, call activation, when it is a B cell, or prolong the life of tissue cells in a host having a T cell that specifically recognises and mediates an immune response directed against the tissue, when it is a killer cell. Specifically, this is useful for preventing transplant (xenograft or allograft) rejection and treating autoimmune disease, e.g. systemic lupus erythematosus, myasthenia gravis, rheumatoid arthritis and insulin dependent diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide amplification using bivalent PCR primer to generate rolling circle intermediate or linear concatemers - requires reduced amt. of primer compared to conventional PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is a component oligonucleotide of the 2.71 kb plasmid plBSfil (Stemmer [1994) Nature 370:389), which encodes the gene and promoter region for R-TEM1 beta-lactamase. A collection of 134 component oligonucleotides, including the present sequence, were synthesised and used to assemble the plasmid by end complementary polymerase reaction (ECPR), employing the overlapping ends of the oilgonucleotides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene; promoter; R-TEM1;
                                                                                                                                                                                                                                                                       Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.9%; Score 21; DB 17; Length 40; 00.0%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   beta-lactamase, construction; assembly, synthesis, end; complementary; polymerase, reaction; ECPR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                ch 0.9%; Score 21; DB 18;
1. Similarity 100.0%; Pred. No. 14;
21; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid p182Sfil component oligonucleotide 40R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 40 BP; 7 A; 13 C; 12 G; 8 T; 0 other;
                                                                                                                                                                                                                         Sequence 36 BP; 8 A; 10 C; 9 G; 9 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide; plasmid; p182Sfil;
                                                                                                                                                                                                                                                                                                                                                         2325 AGCTTGCATGCCTGCAGGTCG 2345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2325 AGCTTGCATGCCTGCAGGTCG 2345
                                                                                                                                                                                                                                                                                                                                                                                                AGCTTGCATGCCTGCAGGTCG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Fig 5C; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95US-0425684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96WO-US05480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT69476 standard; DNA; 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stemmer WPC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-485725/48.
                                                                                                                                                                                                                                                                                       Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lipshutz RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-OCT-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT69476;
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AAT69476
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                                                                                                                                                                                                                                                                     nseq
                                                                                modified or mutated so that it no longer has the pathological effect of a superantigen but is still capable of eliciting an antibody response which cross reacts with and protects against the native superantigen. The TSGT-1 superantigen derivative modifies T-cell receptors or class II major histocompatibility complex (MHC) binding. The superantigen derivative is preferably a deletion or substitution mutation of a portion of the superantigen. The details are a vaccine for preventing and treating antigen-mediated and antigen-initiated diseases. Two primers (AAT27723, AAT27724) were us in the amplification, subcloning and mutagenesis of the toxic shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibiting T cells that recognise preselected target molecules - using killer cells having signal transduction molecule fused to target molecule, useful for inhibiting graft rejection or treating auto-immune disease
                                                                Staphylococcus aureus toxic shock syndrome toxin-1 (TSST-1) is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a primer for the PCR amplification of a cDNA encoding the mouse T cell receptor zeta chain. A novel cell, comprising a signal transduction molecule, preferably a mouse T cell receptor zeta chain, a trached to the extracellular domain (ED) of a major histocompatibility complex (MHC) molecule,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer; polymerase chain reaction; PCR; amplification; mouse; murine; extracellular domain; major histocompatibility complex; MHC; class I; signal transduction; molecule; T cell; receptor; zeta chain; B cell; killer cell; prevention; transplant; xenograft; allograft; rejection; treatment; autoimmune disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      systemic lupus erythematosus; myasthenia gravis;
rheumatoid arthritis; insulin dependent; diabetes mellitus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                DB 17; Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B for mouse T cell receptor zeta chain.
                                                                                                                                                                                                                                                                                                                                                       Sequence 33 BP; 7 A; 9 C; 9 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2325 AGCTTGCATGCCTGCAGGTCG 2345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 38; 157pp; English.
                  Example 2; Page 42; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCTTGCATGCCTGCAGGTCG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT61299 standard; DNA; 36 BP
                                                                                                                                                                                                                                                                                                                                                                                                0.98;
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Matches 21, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-179285/16.
                                                                                                                                                                                                                                                                                                              syndrome toxin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosenberg AS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9708328-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32
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                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Gaps

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The present sequence represents an M13mp18 single stranded DNA probe which was used in a new method for detecting double stranded DNA having a specific DNA nucleotide sequence. The method comprises: (a) mixing the single stranded probe, labelled at the 5' end and with specific nucleotide sequences at its 3' and 5' ends, with the RecA protein molecule; (b) adding a DNA sample containing the double stranded DNA sequence, which is complementary to the specific nucleotide sequences; (c) adding ligase, allowing the nucleotide sequence of the double stranded DNA to overlap with the specific nucleotide sequence at the ends contain and (d) removing the RecA protein molecule, and detecting the resulting hybrid DNA using the label. The method uses to a single stranded DNA probe to detect a double stranded DNA having a specific stranded DNA probe to detect a double stranded DNA having a specific damed of the sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probe; detection; RecA protein; ligase; circular DNA probe; label;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Using single stranded DNA probe to detect double stranded DNA sequence - having specific nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            damage, allowing accurate sequence information to be obtained
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14;
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/note= "Cytosine modified by a label"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AISH-) AISHIN COSMOS KENKYUSHO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M13mp18 single-stranded DNA probe.
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15 AGCTTGCATGCCTGCAGGTCG 35
                                                                                                                                                                                                                                                                                                                         AAT88401 standard; DNA; 40 BP
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modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT88401;
                                                                                                                                                                                          RESULT 15
AAT88401/c
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28 AGCTTGCATGCCTGCAGGTCG 8 В

2325 AGCTTGCATGCCTGCAGGTCG 2345

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0; Gaps

0; Indels

Search completed: November 14, 2003, 11:58:53 Job time : 610.653 secs

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AL986461 Danio rer
AL986536 Danio rer
AL97889 Danio rer
AL978819 Danio rer
AL978910 Danio rer
AL978910 Danio rer
AL973949 Danio rer
AL977007 Danio rer
AL977007 Danio rer
AL97557 Danio rer
AL98425 Danio rer
AL98425 Danio rer
AL98426 Danio rer
AL98406 Danio rer
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AL98718 Danio rer
AL98719 Danio rer
AL98719 Danio rer
AL98714 Danio rer
AL98678 Danio rer
                                                                                                                                                                                                                                                                                                                                                                                                                            UR19H5T 31 bp DNA linear GSS 27-NOV-2002
Danio rerio genomic clone DKEY-19H5, genomic survey sequence.
AL735758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Danio rerio

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

1 (Dases I to 31)

Humphray, S. J.; Huckle, E. and Hunt, S. E.

Direct Submission

Submitted (Os-JNW-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:

humquery@sanger.ac.uk'Unpublished
                                                                                                                                                                                                                                                                                                                                           AL745225 Danio rer
AL743826 Danio rer
AL741484 Danio rer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was generated from the T7 end of BAC 19H5. 19H5 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Keygene.
Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .31
  /organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
                DR48K10T
DR1009T
DR1011T
DR1011T
DR1011T
DR43A1ST
DR43A1ST
DR43A1ST
DR43A1ST
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DR43A1T
DR43A1T
DR43OBT
DR43OBT
DR43OBT
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DR43H15T
DR43L19T
DR43M4T
DR43C7T
DR133T
DR1L3T
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DR43D1T
DR43J7T
DR49M12T
AZ819838
DR43D23T
DR43D23T
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DR43L9T
DR48J2T
AU257958
AU263470
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DR2O22T
DR1L19T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Danio rerio (zebrafish)
 RESULT 1
DR19H5T/C
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
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AL748020 Danio rer
AL983803 Danio rer
AL984851 Danio rer
                                                         2003, 11:17:54 ; Search time 4903.81 Seconds (without alignments) 11686.822 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                              1 ggatcctttcatgtttaaca.....caggtcggaggccaccatgg 2358
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      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                            residues
                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                        OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                           summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DR19H5T
DR6J9T
DR43H24T
DR43J2T
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Gapop_60.0 , Gapext 60.0
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2358
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em_htc: *
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Danio rerio genomic clone DKEY-43B24, genomic survey sequence.
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Danio rerio genomic clone DKEY-43J2, genomic survey sequence.
AL984851
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Direct Submission

Direct Submission

Submitted (14-NoV-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humquery@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 43J2. 43J2 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humquery@sanger.ac.uk Unpublished humquery@sanger.ac.uk Unpublished This sequence was generated from the T7 end of BAC 43H24. 43H24 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 30)
                                                                                  Reygene.
Further details: http://www.sanger.ac.uk/Projects/D_rerio/
Location/Qualifiers
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Location/Qualifiers
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100.0%; Pred. No. 7.8e+02;
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

I (Dases 1 to 31)
Humphray, S. J., Huckle, E. and Hunt, S. E.
Direct Submission

Submitted (06-7UN-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
Hunguery@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 6J9, 6J9 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
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Danic rerio genomic clone DKEY-609, genomic survey sequence.
AL748020
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1 (bases 1 to 30)
Humphray, S. C., Huckle, E. and Hunt, S. E.
Direct Submission
Direct Submission
Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome
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Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
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Danio rerio genomic clone DKEY-48K10, genomic survey sequence.
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Danio rerio genomic clone DKEY-1009, genomic survey sequence.
AL745332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: hungutery@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 48K10. 48K10 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
Humquery@sanger.ac.uk Unpublished
This sequence was generted from the T7 end of BAC 1009. 1009 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
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1 (bases 1 to 31)

Humphray, S.J., Huckle, E. and Hunt, S.E.
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Humphray, S.J., Huckle, E. and Hunt, S.E.
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Further details: http://www.sanger.ac.uk/Projects/D_rerio/
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Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 19; Conservative 0; Mismatches 0;
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1 (bases 1 to 31)

Humphray, S. J., Huckle, E. and Hunt, S. E.

Birect Submission

Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: hunguery@sanger.ac.uk Unpublished

This sequence was generated from the T7 end of BAC 43B24. 43B24 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
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(Syriniformes; Cyprinidae; Danio.

(Dases 1 to 31)

Humphray, S. J., Huckle, E. and Hunt, S. E.

Direct Submission

Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CBIO 1SA, UK. E-mail contact: hunguery@sanger.ac. uk Unpublished

This sequence was generated from the T7 end of BAC 43B2: 43B2 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
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Danio rerio genomic clone DKEY-43B2, genomic survey sequence.
AL986536
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Location/Qualifiers
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ative 0; Mismatches 0;
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/note="Vector pIndigoBAC-536"
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    AL986461.1 GI:25184019
GSS.
                                                   Danio rerio (zebrafish)
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Best Local Similarity 100.
Matches 19; Conservative
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VERSION
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Direct Submission Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: hunguery@sanger.ac.uk Unpublished This sequence was generated from the T7 end of BAC 1N11. 1N11 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
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Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humquery@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 43F16, 43F16 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
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1 (bases 1 to 33)

Humphray, S.J., Huckle, E. and Hunt, S.E.
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Danio rerio genomic clone DKEY-43F16, genomic survey sequence.
AL975436
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Location/Qualifiers
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Pred. No. 2.5e+03;
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100.0%; Pred. No. 2.5e+03;
cive 0; Mismatches 0;
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100.0%; Pred. No. ...
0; Mismatches
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/mol_type="genomic DNA"
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1 (bases 1 to 30)

Humphray, S. J., Huckle, E. and Hunt, S. E.

Direct Submission

Submitted (14-NOv-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CBIO 1SA, UK. E-mail contact: Hunguery@sanger.ac.uk Unpublished

This sequence was generated from the T7 end of BAC 42M15. 42M15 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
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Danio rerio genomic clone DKEY-lN11, genomic survey sequence.
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Danio rerio genomic clone DKEY-42M15, genomic survey sequence.
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1 (bases 1 to 32)
Humphray, S. J., Huckle, E. and Hunt, S. E.
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Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 7.8s
Matches 19; Conservative 0; Mismatches
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/organism="Danio rerio"
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Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
humquery@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 35H17. 35H17 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail contact:
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1 (bases 1 to 37)

Humphray, S. J., Huckle, E. and Hunt, S. E.
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Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hunduer/@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 43P8. 43P8 is
part of the Daniokey BAC Library created by R. Plasterk and N.V.
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Danio rerio genomic clone DKEY-35H17, genomic survey sequence.
AL975957
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Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
Location/Qualifiers
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Further details: http://www.sanger.ac.uk/Projects/D_rerio/
Location/Qualifiers
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.00.0%; Pred. No. 2.5e+03;
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Humphray, S.J., Huckle, E. and Hunt, S.E.
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                       0; Mismatches
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DR35H17T/c
                       Matches
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DR43P8T/c
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AUTHORS
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Gypriniformes; Cyprinidae; Danio.

1 (bases 1 to 35)

Humphray, S. J., Huckle, E. and Hunt, S. E.

Direct Submission

Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CBIO 1SA, UK. E-mail contact: humquery@sanger.ac.uk Unpublished

This sequence was generated from the T7 end of BAC 10P1. 10P1 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
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Cypriniformes; Cyprinidae; Danio.

Humphray, S. J., Huckle, E. and Hunt, S. E.

Birect Submission

Submitted (14-NOV-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: Hunguery@sanger.ac.uk Unpublished

This sequence was generated from the T7 end of BAC 43A15. 43A15 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
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Danio rerio genomic clone DKEY-43A15, genomic survey sequence.
AL973794
Danio rerio genomic clone DKEY-10P1, genomic survey sequence.
AL737949
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Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
Location/Qualifiers
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Location/Qualifiers
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100.0%; Pred. No. 2.5e+03;
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Query Match 0.8%; Score 18; DB 29; Length 43; \*Best Local Similarity 100.0%; Pred. No. 2.60+03; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps

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Search completed: November 14, 2003, 19:05:45 Job time : 4906.81 secs

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Sequence 7197, Pp. Paragraph Patent No. 5508178 Patent No. 5508178 Sequence 5, Appli Sequence 4, Appli Sequence 48, Appli Sequence 48, Appli Sequence 48, Appli Sequence 46, Appli
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233 South Wacker Drive, 6300 Sears Tower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lockerbie, Robert Owen, et al.
TITLE OF INVENTION: Calcineurin Inhibitory Compounds
TITLE OF INVENTION: and Anchoring Protein
NUMBER OF SEQUENCES: 74
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & B
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: HELLER, MICHAEL J.
APPLICANT: TU, EUGENE
TITLE OF INVENTION: DNA OPTICAL STORAGE
FILE REFERENCE: DAVID B. WURPHY - Heller 236/119
CURRENT APPLICATION NUMBER: US/09/129,740A
CURRENT FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 08/906,569
EARLIER FILING DATE: 1997-08-05
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATCHIN Ver. 2.0
US-09-129-740-14
US-09-661-026-29
US-09-568-52-14
US-09-230-180-13
US-09-230-180-13
US-09-22-978-7197
5508178-9
5508178-8
5508178-8
US-08-51-8
US-08-721-4588-47
US-08-721-4588-46
US-08-300-582-1
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Pred. No. 1.9;
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STATE: Illinois
COUNTRY: United States of America
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
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Sequence 45, Application US/08721458B

Patent No. 6107104

GENERAL INFORMATION:
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LENGTH: 30
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ORGANISM: 6
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Sequence 11,
Sequence 1, A
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(cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/RB_COMB.seq:*
/cgn2_6/ptodata/2/ina/RB_COMB.seq:*
/cgn2_6/ptodata/2/ina/RB_CTUS_COMB.seq:*
                5.1.6
Compugen Ltd.
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US-08-721-458B-45

US-09-423-792-11

US-09-423-792-11

US-09-68-527-15

US-09-267-574-11

US-09-267-574-11

US-09-081-576-2

US-09-081-576-2

US-09-091-576-2

US-09-091-576-2

US-09-025-045-4

US-09-039-045-144A-8

US-09-455-144A-8

US-09-455-144A-8

US-08-455-144A-8

US-08-455-144A-8

US-08-455-147-8

US-08-455-147-8

US-08-675-502-78

US-08-675-502-78

US-08-675-502-78

US-08-675-502-78

US-08-675-502-78

US-08-675-502-78

US-08-675-502-78

US-08-675-502-78

US-08-675-502-78
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US-08-585-593A-58
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US-09-921-203-2
                                                                                                                                                                                                                                                                                             569978 segs, 220691566 residues
                    version :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Listing first 45 summaries
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                                                                                                                                                                                                                                          OLIGO_NUC
Gapop_60.0 , Gapext 60.0
                  GenCore
Copyright (c) 1993
                                                                                                                                                                            US-10-005-337A-1
2358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 50
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Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                                                                                              Scoring table:
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OTHER INFORMATION: synthetic oligonucleotide template of M13-30

CHER INFORMATION: complementary to the synthesized sequence

18-09-423-742-1
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US-08-877-599-11/C
US-08-877-599-11/C
Sequence 11, Application US/08877599
; Patent No. 6372212
; GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Chitinase Materials and Methods
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Born
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                 Score 21; DB 3; Length 30;
Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 30;
                                                                                                                                                                                                                 0; Indels
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STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.9%; Score 21; DB 4;
100.0%; Pred: No. 1.9;
tive 0; Mismatches
                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INVOCATIONS

APPLICANT: Kwiatkowski, Marek
APPLICANT: Landegren, Ulf
APPLICANT: Nilsson, Mats
TILLE OF INVENTION: SOLID PHASE SYNTHESIS
FILE REFERENCE: 11989-005001
CURRENT APPLICATION NUMBER: US/09/423,742
CURRENT FILING DATE: 1999-11-12
PRIOR FILING DATE: 1998-05-14
PRIOR FILING DATE: 1998-05-14
PRIOR FILING DATE: 1998-05-14
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2325 AGCTTGCATGCCTGCAGGTCG 2345
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                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 1, Application US/09423742; Patent No. 6313284; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                             29 AGCTTGCATGCCTGCAGGTCG 9
                                                                                                                                                               Query Match 0.9%; Sc
Best Local Similarity 100.0%; P
Matches 21; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 21; Conservative
30 base pairs
                      TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
US-09-423-742-1/c
                                                                                                                  US-09-039-198A-11
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LENGTH: 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.9%; Score 21; DB 3; Length 30; 100.0%; Pred. No. 1.9; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Gray, Patrick W.
APPLICANT: Tjoelker, Larry W.
TITLE OF INVENTION: CHITINASE CHITIN-BINDING FRAGMENTS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PLEATION NUMBER: US/09/039,198A
FILING DATE:
PatentIn Release #1.0, Version #1.25
                                                                                  FILING DATE:
CLASSTRICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/404,731
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/344,227
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/503,226
FILING DATE: 17-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAMM: Williams Dr. JOSEPH A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 312-674-6300
TELEPHONE: 312-474-6300
INPORMATION FOR SEQ ID NO: 45:
ENGURNE CHARACTERISTICS:
LENGTH: 30 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Heien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27866/34391
TELECOMMUNICATION INFORMATION:
TELEPRAK: (312) 474-6300
TELEFAX: (312) 474-6468
INFORMATION FOR SEQ ID NO: 11:
                                            US/08/721,458B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2325 AGCTTGCATGCCTGCAGGTCG 2345
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Best Local Similarity 100.
Matches 21; Conservative
                 CURRENT APPLICATION DATA APPLICATION NUMBER: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 11
MOLECULE TYPE:
                                                                        FILING DATE:
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  SOFTWARE:
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; OTHER INFORMATION: Description of Artificial Sequence: primer US-09-267-574-11
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Pred. No. 1.9;
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GENERAL INFORMATION:
APPLICANT: PHILLIP MARRACK
APPLICANT: RICHARD SHIMONKEVITZ
APPLICANT: RICHARD SHIMONKEVITZ
APPLICANT: RICHARD SHIMONKEVITZ
APPLICANT: MASAZUMI MATSUMURA
TITLE OF INVENTION: SUPERANTIGENS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                          Query Match 0.9%; Score 21; DB 4; Best Local Similarity 100.0%; Pred. No. 1.9; Matches 21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09081576A
Fatent No. 6180111
GENERAL INFORMATION:
APPLICANT: STEIN, Daniel C.
TITLE OF INVENTION: VACCINE DELIVERY SYSTEM
FILE REPRENCE: 2747-0097-27 (IP (8014-014))
CURRENT APPLICATION NUMBER: US/09/081,576A
CURRENT PILING DATE: 1998-05-19
FRIOR APPLICATION NUMBER: US 08/936,522
FRIOR FILING DATE: 1997-09-23
FRIOR FILING DATE: 1995-05-18
FRIOR APPLICATION NUMBER: US 08/443,514
FRIOR FILING DATE: 1995-05-18
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Swanson & Bratschun, L.L.C.
8400 E. Prentice Ave., Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. ...
      EARLIER APPLICATION NUMBER: 09/039,198
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MEDIUM TYPE: Diskette, 3.5 inch
                                                                                                                                                                                                                                                                                                                                                                          29 AGCTTGCATGCCTGCAGGTCG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 AGCTTGCATGCCTGCAGGTCG 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Neisseria gonorrhoeae
US-09-081-576-2
                      EARLIER FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.9
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Englewood
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US95-14639-3/c
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ZIP: 80111
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                                                                                     SEQ ID NO 11
LENGTH: 30
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LENGTH: 32
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Patent No. 6399571
GENERAL INFORMATION:
APPLICANT: Gray, Patrick W.
APPLICANT: Tjoelker, Larry W.
TITLE OF INVENTION: CHITINASE CHITIN-BINDING FRAGMENTS
FILE REFERENCE: 27866/35407
CURRENT APPLICATION NUMBER: US/09/267,574
CURRENT FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Application US/0956857

Patent No. 6385080

GENERAL INFORMATION:

APPLICANT: HELLER, MICHAEL J.

APPLICANT: TU, EUGENE

TITLE OF INVENTION: DNA OPTICAL STORAGE

FILE REPERRACE: DAVID B. WIRPHY - Heller 253/078

CURRENT FILING DATE: 2000-05-09

PRIOR FILING DATE: 1998-08-05

WINDER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.9%; Score 21; DB Best Local Similarity 100.0%; Pred. No. 1.9 Matches 21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Pred. No. 1.5
tive 0; Mismatches
                               CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PPLICATION NUMBER: US 08/663,618
FILING DATE: 14-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27866/33994
TELECHONE: 312/474-6300
US/08/877,599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2325 AGCTTGCATGCCTGCAGGTCG 2345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: synthetic construct US-09-568-527-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Ver. 2.0
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Best Local Similarity 100.0
Matches 21; Conservative
                                                                                                                                                                                                                                                                            TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                        312/474-0448
                                                                                                                                                                                                                                                                                                                                               30 base pairs
                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-267-574-11/c
                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
US-09-568-527-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-877-599-11
                                                                                                                                                                                                                                                        TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PROPERTY SEQ ID NO 15
LENGTH: 30
                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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Sequence 4, Application US/09435221'

Patent No. 6491908

GENERAL INFORMATION:
APPLICANT: Rosenberg, Amy Sonya

TITLE OF INVENTION: Selective Elimination of T Cells That
Recognize Specific Preselected Targets
                                                                                                                                                          Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 36;
                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 015280-236100US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/029,045
FILING DATE: 02-JUN-1998
APPLICATION NUMBER: US 60/002,964
FILING DATE: 30-AUG-1995
APPLICATION NUMBER: WO PCT/US96/13873
FILING DATE: 29-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.9%; Score 21; DB 4;
100.0%; Pred. No. 1.9;
tive 0; Mismatches
                                                                                                                                                                                                       Mismatches
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REPLICATION NUMBER: US/09/435,321
FILING DATE: 04-No. 6491908-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear

MOLECULE TYPE: DIA

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-435-321-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Weber, Kenneth A. REGISTRATION NUMBER: 31,677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2325 AGCTTGCATGCCTGCAGGTCG 2345
                                                                                                                                                                                                                                                   2325 AGCTTGCATGCCTGCAGGTCG 2345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (415) 576-0200
(15) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 AGCTTGCATGCCTGCAGGTCG 34
                                                                                                                                                                                                                                                                                            14 AGCTTGCATGCCTGCAGGTCG 34
                                                                                                                                               0.9%; Scor
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 4:
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Best Local Similarity 100.
Matches 21, Conservative
                                                                                                                                                                                 Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (415)
                               TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                    linear
                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA
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                                                                                                                   US-09-029-045-4
                                                                                                                                                                 Query Match
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Patent No. 6056952
GENERAL INFORMATION:
APPLICANT: Rosenberg, Amy Sonya
TITLE OF INVENTION: Selective Elimination of T Cells That
TITLE OF INVENTION: Recognize Specific Preselected Targets
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5; Length 33;
1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: UGA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/029,045
FILING DATE: 02-UN-1998
CLASSITCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,964
FILING DATE: 30-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/13873
FILING DATE: 29-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 015280-236100US
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew LL STREET: Two Embarcadero Center, Eighth Floor CITY: San Prancisco
OPERATING SYSTEM: MS-DOS
SOPTWARE: WOrdPerfect 6.0 for windows
CURRENT APPLICATION DATA:
CLASSIFICATION NUMBER: PCT/US95/14639
FILING DATE:
CLASSIFICATION DATA:
RAPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/338,373
FILING DATE: 14-November: 1994
ATTORNEY/AGENT INFORMATION:
NAME: BATTY J. SWANSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.9%; Score 21; DB 100.0%; Pred. No. 1.9 Live 0; Mismatches
                                                                                                                                                                                                                                                                         SUP020/PCT
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                                                                                                                                                                                                                          NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: SUPOZ
TELECOMMUNICATION INPORMATION:
TELEPHONE: (303) 793-3433
INPORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            California
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US-09-029-045-4
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ATTORNEY/AGENT INFORMATION:
NAME: DUNN ESQ., TRACY J.
REGIGSTRATION NUMBER: 34,587
REFRENCE/DOCKET NUMBER: 165
TELECOMMUNICATION INPORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34,587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                        Sailland, Alain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.9
Best Local Similarity 100.
Matches 21; Conservative
    Lebrun, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U.S.A.
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US-08-425-684-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-08-425-684-78
                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-945-144A-8
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APPLICANT: DEROSE, Richard

APPLICANT: DEROSE, Richard

APPLICANT: DEROSE, Richard

APPLICANT: DEROSE, Richard

APPLICANT: GIGOT, Claude (deceased)

TITLE OF INVENTION: ELEMENT IN A CHIMMERIC GENE WHICH CAN BE USED FOR THE

TITLE OF INVENTION: ELEMENT IN A CHIMMERIC GENE WHICH CAN BE USED FOR THE

TITLE OF INVENTION: TRANSFORMATION OF PLANTS

FILE REFERENCE: 022650-453

CURRENT APPLICATION NUMBER: US/09/000,062

CURRENT FILING DATE: 1996-07-17

EARLIER PILING DATE: 1996-07-17

EARLIER PILING DATE: 1996-07-19

NUMBER OF SEQ ID NOS: 22

CONTRARE: PATELING DATE: 1995-07-19
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                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: MedC modified OTHER INFORMATION: complement to plasmid pMS19
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100.0%; Pred. No. 1.9;
ive 0; Mismatches 0; Indels
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Pred: No. 1.9;
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                                                                        APPLICANT: Wetmur, James G
APPLICANT: Wetmur, Robin S
APPLICANT: Wetmur, Robin S
APPLICANT: Brogalhardt, Dean L
TITLE OF INVENTION: Branch Migration of Nucleotides
FILE REFERENCE: BNZ-49(P) (C) SEQUENCES
CURRENT APPLICATION NUMBER: US/09/387,300
CURRENT FILING DATE: 1999-08-31
BARLIER APPLICATION NUMBER: 08/480,000
EARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 39
LENGTH: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pred: No.
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           Sequence 39, Application US/09387300 Patent No. 6358685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/09000062 Patent No. 6338961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 AGCTTGCATGCCTGCAGGTCG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 8, Application US/08945144A
                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.9%;
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Best Local Similarity 100.0
Matches 21; Conservative
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Best Local Similarity
Matches 21; Conserva
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US-09-000-062-11
                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JS-09-000-062-11/c
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US-08-945-144A-8/c
-09-387-300-39
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Synthase,
APPLICANT: Freyssinet, Georges
APPLICANT: DeGryse, Eric
TITLE OF INVENTION: Mutated 5-Enol Pyruvylehikimate-3-Phosphate Synthase
TITLE OF INVENTION: Gene Coding for Said Protein and Transformed Plants
TITLE OF INVENTION: Containing Said Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: TOWNSEND AND TOWNSEND AND CREW ONE MARKET PLAZA, STEUART STREET TOWER, 20TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: STEMMER PH.D., WILLEM P.C.
TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
NUMBER OF SEQUENCES: 136
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
STREET: ONE MARKET PLAZA, STEUART STREET TOWER, 20TH FLC
CITY: SAN FENCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 21; DB 4; Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/425,684
FILING DATE: 18-APR.1995
CLASSIFICATION: 435
                                                                                            CURRENT APPLICATION NUMBER: US/08/945,144A
CURRENT FILING DATE: 1998-01-20
PRIOR APPLICATION NUMBER: US/08/945,144A
CURRENT FILING DATE: 1998-01-20
PRIOR APPLICATION NUMBER: FRANCE 95/08979
PRIOR FILING DATE: 1996-07-18
PRIOR FILING DATE: 1995-07-19
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 8
LENGTH: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Prec. ...
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0; Gaps 0; Indels Best Local Similarity 100.0%; Pred. No. 1.9; Matches 21; Conservative 0; Mismatches

0;

. 2325 AGCTTGCATGCCTGCAGGTCG 2345

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Search completed: November 14, 2003, 16:31:52 Job time : 136.074 secs

Sequence 25, Appl Sequence 26, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 2, Appli Sequence 20, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 20, Appl Sequence 20, Appl

Seguence Seguence Sequence

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Title: Perfect score:

Seguence:

OM nucleic

Run on:

Scoring table:

Minimum DB Maximum DB

Database

Word size Searched:

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Sequence 26, Application US/10086464
; Sequence 26, Application US/10086464
; Publication No. US20020199218A1
; GENERAL INFORMATION:
    APPLICANT: GORING, Daphe R. et al.
    TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
    FILE REFERENCE: P 25, 762-A USA
    CURRENT APPLICATION NUMBER: US/10/086,464
; CURRENT PILING DATE: 2002-02-28
    FRIOR APPLICATION NUMBER: US 10/069,304
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/149,466
; PRIOR FILING DATE: 1999-08-19
; PRIOR PILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 26
; FROM ARE REALISED APPLICATION NUMBER: US 60/159,122
; NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 26
; FROM ARE REALISE PARCHLIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: primer US-10-086-464-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.9%; Score 21; DB 13; Length 27; Best Local Similarity 100.0%; Pred. No. 6.6; Matches 21; Conservative 0; Mismatches 0; Indels
      US-09-231-235-25
US-09-797-518A-25
US-10-131-591A-56
US-10-131-591A-56
US-10-131-591A-100
US-10-128-597-110
US-10-128-597-111
US-10-128-597-111
US-10-021-237-2
US-09-949-477-109
US-10-085-906-78
US-10-085-906-78
US-10-085-906-6
US-09-940-244-20
US-09-940-244-20
US-09-941-193A-20
US-09-941-193A-20
US-09-941-193A-20
US-09-941-193A-20
US-09-941-193A-20
US-09-941-193A-20
US-09-941-193A-20
US-09-941-193A-20
US-10-081-866-20
US-10-081-866-20
US-10-081-866-20
US-10-081-866-20
US-10-081-866-20
US-10-081-866-20
                                                                                                                                                                                                                                                                                                                 US-09-995-593A-38
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US-10-170-172-41
US-09-940-244-19
                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
US-10-086-464-26
FEATURE:
000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Appl
Sequence 78, Appl
Sequence 161, App
Sequence 161, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 2, Appl
Sequence 252, Appl
Sequence 252, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Appli
Sequence 11, Appl
Sequence 2, Appli
                                                                                   November 14, 2003, 11:39:49 ; Search time 711.869 Seconds (without alignments) 10825.622 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 26, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                    2358
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                                                                                                                                                                 1 ggatcctttcatgtttaaca.....caggtcggaggccaccatgg
                                                                                                                                                                                                                                                                                                                                                                           Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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         5.1.6
Compugen Ltd.
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US-09-95-944-1
US-10-161-547-11
US-10-023-839-11
US-09-940-925-161
US-09-940-925-161
US-09-941-193A-161
US-09-341-193A-161
US-09-341-193A-161
US-09-231-235-10
US-09-291-235-10
US-09-996-073-8
                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                   2169961 segs, 1634102185 residues
          GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                      Post-processing: Listing first 45 summaries
                                                             sw model
                                                                                                                                                                                          OLIGO NUC
Gapop_60.0 , Gapext 60.0
                                                            nucleic search, using
                                                                                                                                       US-10-005-337A-1
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Match Length
                                                                                                                                                                                                                                                                                                               seq length: 0 seq length: 50
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Gaps

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2325 AGCTTGCATGCCTGCAGGTCG 2345 AGCTTGCATGCCTGCAGGTCG 25

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Score

Result No.

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RESULT 2 US-09-952-944-1/c

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TYPE: DNA ORGANISM: Zea mays
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US-09-245-802-78
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                                                                                                                                                                                                                                                                                                                                                                                       US-10-153-902-2
                                                                                                                                                                                                                                                                                                  SEC ID NO 2
                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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Sequence 11, Application US/10161547

Publication No. US20030143216A1

Publication No. US20030143216A1

APPLICANT: Gray, Patrick W.

APPLICANT: Tjoelker, Larry W.

TILLE OF INVENTION: CHITINASE CHITIN-BINDING FRAGMENTS

FILE REPERENCE: 27866/35407

CURRENT APPLICATION NUMBER: US/10/161,547

CURRENT PILING DATE: 2002-06-03

PRIOR FILING DATE: 1999-03-12

PRIOR FILING DATE: 1999-03-12

PRIOR FILING DATE: EARLIER PILING DATE: 1998-03-12

NUMBER OF SEQ ID NOS: 39

SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: synthetic oligonucleotide template of M13-30 OTHER INFORMATION: complementary to the synthesized sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.9%; Score 21; DB 12; Length 30; ilarity 100.0%; Pred. No. 6.6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 9;
6.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.9%; Score 21; DB Best Local Similarity 100.0%; Pred. No. 6.6 Matches 21; Conservative 0; Mismatches
                                                            APPLICANT: Kwistlowski, Marek
APPLICANT: Landegren, Ulf
APPLICANT: Landegren, Ulf
APPLICANT: Nilsson, Mates
APPLICANT: Nilsson, Mates
FILE REFERENCE: 11989-005001
CURRENT APPLICATION NUMBER: US/09/952,944
CURRENT APPLICATION NUMBER: US/09/423,742
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1997-05-14
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2325 AGCTTGCATGCCTGCAGGTCG 2345
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Sequence 1, Application US/09952944
Patent No. US20020051994A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2325 AGCTTGCATGCCTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 21; Conserv
                                              GENERAL INFORMATION:
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Sequence 11, Application US/10023839

Publication No. US20030027312A1

Publication No. US20030027312A1

Sequence 11, Application No. US20030027312A1

APPLICANT: DEROSE, Richard

APPLICANT: CHAUBET, Nicole

APPLICANT: GENEWHICH CAN BE USED FOR THE

TITLE OF INVENTION: TRANSFORMATION OF PLANTS

FILLE OF INVENTION: TRANSFORMATION OF PLANTS

FILLE APPLICATION NUMBER: US/10/023,839

CURRENT APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US/09/000,062

PRIOR FILLING DATE: BARLIER FILLING DATE: 1998-05-29

PRIOR FILLING DATE: EARLIER FILLING DATE: 1998-05-29

PRIOR FILLING DATE: EARLIER FILLING DATE: 1998-05-29

NUMBER OF SEQ ID NOS: 22

SOSTWARE PATENTIN OF NOWER.
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APPLICANT: STEMMER PH.D., WILLEM P.C.
APPLICANT: LIPSHUTZ, ROBERT J.
TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
NUMBER OF SEQUENCES: 136
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 21; DB 14; Length 38;
Pred. No. 6.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 21; DB 13; Length 32;
Pred. No. 6.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
PRILE OF INVENTION: VACCINE DELIVERY SYSTEM FILE REFERENCE: 2747-0097-27 CIP (8014-014) CURRENT APPLICATION NUMBER: US/10/153,902 CURRENT FILING DATE: 2002-05-24 PRIOR APPLICATION NUMBER: US/09/081,576 PRIOR PILING DATE: 1998-05-19 PRIOR PAPLICATION NUMBER: US/09/081,576 PRIOR PAPLICATION NUMBER: US 08/936,522 PRIOR FILING DATE: 1999-05-23 PRIOR PILING DATE: 1999-05-18 PRIOR PLING DATE: 1995-05-18 NUMBER: OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Preu. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2325 AGCTTGCATGCCTGCAGGTCG 2345
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Patent No. US20010049125A1
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Best Local Similarity 100.0%; P:
Matches 21; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.9%;
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Best Local Similarity
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Sequence 2, Application US/10153902 Publication No. US20020187160A1 GENERAL INFORMATION:

US-10-153-902-2/c

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Publication No. US20030108873A1
GENERAL INPORMATION:
APPLICANT: BROW, MARY ANN D.
LYAMICHEV, VICTOR I.
OLIVE, DAVID M.
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.9%; Score 21; DB 11; Length 46; Best Local Similarity 76.2%; Pred. No. 6.6; Matches 16; Conservative 5; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                        ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01756
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: UNITED STATES OF AMERICA ZIP: 94104
                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: RNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 161: US-09-940-925A-161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: RNA (genomic)
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SEQUENCE DESCRIPTION: SEQ ID NO: 161:
US-09-941-193A-161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2325 AGCTTGCATGCCTGCAGGTCG 2345
                                                                                                                                 TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 AGCUUGCAUGCCUGCAGGUCG 30
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                                                                                                                                                                                                                           LENGTH: 46 base pairs
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LENGTH: 46 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                        TELEFAX: (415) 397-83
INFORMATION FOR SEQ ID NO: 161:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 161
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CORRESPONDENCE ADDRESS:
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TELEFAX: (415) 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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LYAMICHEV, VICTOR I.
OLIVE, DAVID M.
TITLE OF INVENTION: RAFID DETECTION AND IDENTIFICATION OF PATHOGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/940,925A
FILING DATE: 10-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.9%; Score 21; DB 9; Length 40; Best Local Similarity 100.0%; Pred. No. 6.6; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO STATE: CALIFORNIA
                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/245,802
                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05480
FILING DATE: 18-APR-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY, ESQ., MATTHEW B.
REGISTATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 16528J-015410US
TELECOMMUNICATION INFORMATION:
ISEE: TOWNSEND AND TOWNSEND AND CREW
: TWO EMBARCADERO CENTER, BTH FLOOR
SAN FRANCISCO
CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 161, Application US/09940925A Publication No. US20030054338A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2325 AGCTTGCATGCCTGCAGGTCG 2345
                                                                                                                                                                                                  PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/675,502
                                                                                       TELEPAONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 78: SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  circular
                                                                                                                                                                       COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
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  ADDRESSEE:
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Matches

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sneridan, Philip Lee
...rutCANT: Hardy, Steven

APPLICANT: Dubensky, Thomas
APPLICANT: Yee, Jing-Kun

TITLE OF INVENTION: FELINE IMMUNOBERICIENCY VIRUS GENE THERAPY VECTORS
FILE REFERENCE: 930.049.467

CURRENT APPLICATION NUMBER: US/09/797,518A

CURRENT FILING DATE: 2001-03-01

PRIOR FILING DATE: 1999-01-15

NUMBER OF SEQ ID NOS: 63

SOFTWARE: Patentin Ver. 2.0

LENGTH: 24

TYPE: ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: GASMI, Mehdi
APPLICANT: GASMI, Mehdi
APPLICANT: SAUTER, Sybille
TITLE OF INVENTION: FUNCTIONAL LENTIVIRAL VECTOR FROM
TITLE OF INVENTION: AN MLV-BASED BACKBONE
FILE REFERENCE: 2302-1642 / 1642.002
CURRENT APPLICATION NUMBER: US/09/996,073
CURRENT FILING DATE: 2001-11-27
SOFTWARE: PATENTIN VOS: 34
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22;
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                                                                                                                         Sequence 10, Application US/09797518A; Patent No. US20020068354A1
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Publication No. US2030003565A1
GENERAL INFORMATION:
APPLICANT: DUBENSKY JR., Thomas W.
                    5 GGGAGCTTGCATGCCTGCAG 24
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Best Local Similarity
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LENGTH: 24
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APPLICANT: Johnston, Julie C.
APPLICANT: Sauter, Sybille L.
APPLICANT: Sauter, Subille L.
APPLICANT: Sheridan, Philip Lee
APPLICANT: Beridan, Philip Lee
APPLICANT: Dubensky, Thomas
APPLICANT: Vee, Jing Kuan
TITLE OF INVENTION: FELLNE IMMUNODEFICIENCY VIRUS GENE THERAPY VECTORS
FILE REFERBNCE: 930049.467
CURRENT APPLICATION NUMBER: US/09/231,235
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
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22;
Indels
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; OTHER INFORMATION: Primer Used in Examples 2A and 2B
US-09-231-235-10
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5; Mismatches
                                                                                                                                                                                                                                                        APPLICANT: Kwietkowski, Marek
APPLICANT: Landegren, Ulf
APPLICANT: Landegren, Ulf
APPLICANT: Landegren, Ulf
APPLICANT: Landegren, Ulf
TITLE OF INVENTION: SOLID PHASE SYNTHESIS
FILE REFERENCE: 11989-06001
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: 09/254,048
PRIOR FILING DATE: 1999-07-19
PRIOR FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; OTHER INFORMATION: circularization probe
US-10-106-832-2
                                         2325 AGCTTGCATGCCTGCAGGTCG 2345
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                                                                                                                                                                                              Sequence 2, Application US/10106832
Publication No. US20020177698A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
Conservative
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US-10-106-832-2/c
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LENGTH: 50
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Query Match
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              Sequence 10, Application US/09872696A

Publication No. US20030104611A1

GENERAL INFORMATION;

APPLICANT: Johnston, Julie C.

APPLICANT: Hau, David

APPLICANT: Hau, David

APPLICANT: Hau, David

APPLICANT: Havdy, Steven

APPLICANT: Pubensky, Thomas

APPLICANT: Vee, Jilng-Kuan

TITLE OF INVENTION: FELINE IMMUNOBEFICIENCY VIRUS GENE THERAPY VECTORS

FILE REFERENCE: 930049.467

CURRENT APPLICATION NUMBER: US/09/872,696A

CURRENT FILING DATE: 1999-01-18

NUMBER OF SEQ ID NOS: 63

SOFTMARE: PATENTIN VET. 2.0
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OTHER INFORMATION: Description of Artificial Sequence: Primer
OTHER INFORMATION: Primer Used in Examples 2A and 2B
US-09-872-696A-10
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Publication No. US20030082149A1

GENERAL INFORMATION:

APPLICANT: Rowe, David W.

APPLICANT: Stover, Mary Louise

APPLICANT: Beckley, Akin

TITLE OF INVENTION: WITH A MODIFIED UI SMALL NUCLEAR RNA

TITLE OF INVENTION: WITH A MODIFIED UI SMALL NUCLEAR RNA

TITLE OF INVENTION: WITH A MODIFIED UI SMALL NUCLEAR RNA

TITLE OF INVENTION: WITH A MODIFIED UI SMALL NUCLEAR RNA

FILE REPERENCE: UCT97-02PA

CURRENT APPLICATION NUMBER: US/09/123,064

CURRENT FILING DATE: 1998-07-27

EARLIER PILING DATE: 1998-07-28

NUMBER OF SEQ ID NOS: 6

SEQ ID NOS: 6

LENGTH: 28
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 20; Conservative
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-09-872-696A-10
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LENGTH: 24
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RESULT 15 US-09-949-427-252

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Sequence 252, Application US/09949427;
Publication No. US20030054418A1
GENERAL INPOMATION:
APPLICANT: Bodnar, Jackie S.
APPLICANT: Castellan; Lawrence W.
APPLICANT: Lusis, Aldons J.
APPLICANT: Add Jones, Darier
APPLICANT: Add Consol. Darier
CURRENT APPLICANT: WHOWER: US/09/949,427
FILE REFERENCE: 0201.0014.NPUSD.
CURRENT FILING DATE: 2001.09-07
FILE REFERENCE: 0201.09-07
FRIOR APPLICATION NUMBER: 60/231,322
CURRENT FILING DATE: 2000.09-07
FRIOR APPLICANTION NUMBER: 60/231,322
CURRENT FILING DATE: 2000.09-07
FRIOR APPLICANTION NUMBER: 05/210-07
FRIOR APPLICANTION NUMBER: 05/210-07
FRIOR APPLICANTION NUMBER: 06/231,322
FRIOR APPLICANTION NUMBER: 06/231,322
CURRENT FILING DATE: 2001.09-07
FRIOR APPLICANTION NUMBER: 06/231,322
CURRENT FILING DATE: 2001.09-07
FRIOR APPLICANTION: Synthetic Primer
US-09-949-427-252
Query Match
Best Local Similarity 100.0%; Pred. No. 72;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0
1 CTTGCATGCAGGTGG 2345
Db 1 CTTGCATGCAGGTGG 19
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Search completed: November 14, 2003, 19:28:14 Job time: 715.869 secs

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AX004499 Sequence AR106883 Sequence AR293216 Sequence AX484404 Sequence AR290608 Sequence AR290806 Sequence U08249 Human chrom

X12653 Mouse Hox-3

AR041401 Sequence AR041402 Sequence AR041409 Sequence AR041410 Sequence

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sullivan, S.M. and Draper, K.G.
Ribozymes trargeted to TNF-.alpha. RNP
Patent: US 5616490-A 29 01-APR-1997;
Location/Qualifiers
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Sequence 29 from patent US 5616490.
139756
139756.1 GI:2084216
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                                          SUMMARIES
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ORGANISM
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          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Perfect score:
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PAT 13-MAY-1997

linear

AR224513 Sequence AR228975 Sequence AR242931 Sequence AX384983 Sequence BD105584 Genes sen I76944 Sequence 3

AX637411 Sequence AX72294 Sequence AX73859 Sequence A83584 Sequence 13 A8359 Sequence 27 AR004674 Sequence AR00160 Sequence AR136943 Sequence

AX636880 Sequence AX637393 Sequence AX637395 Sequence AX637397 Sequence AX637401 Sequence AX637411 Sequence

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BASE COUNT

ORIGIN

RESULT 2 AX084499/c

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DEFINITION

ACCESSION VERSION

KEYWORDS

SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL

TITLE

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PAT 16-AUG-2002
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                                                                                    PAT 12-JUN-2003
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                            a high density
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roemer, T., Jiang, B., Boone, C., Bussey, H. and Ohlsen, K.L. Gene disruption methodologies for drug target discovery Patent: WO 0205378-A 1704 11-JUL-2002; Elitra Pharmaceuticals, Inc. (US)
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100.0%; Pred. No. 2.2e+04;
ive 0; Mismatches 0; Indels
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Cohen,D., Chumakov,I. and Blumenfeld,M.
Biallelic markers for use in constructing
disequilibrium map of the human genome
patent: US 6537751-A 4951 25-MAR-2003;
                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 0.8%; Score 16; DB 6; Le Best Local Similarity 100.0%; Pred. No. 2.3e+04; Matches 16; Conservative 0; Mismatches 0;
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/organism="Candida albicans"
/mol_type="genomic DNA"
/db_xref="taxon:5476"
? a 5 c 1 g 25 t
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Sequence 2343 from patent US 6537751.
AR290608 AR290608.1 GI:31677892
                                                                           19 bp DN Sequence 4951 from patent US 6537751. AR293216 AR293216.1 GI:31680500
                                                                                                                                                                                                                                                                                                                                               /organism="unknown"
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1 ACCATCCACTGACTGA 16
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Best Local Similarity 100.0
Matches 16; Conservative
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Unclassified.
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AR290608
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Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                               Blackshear, P.J., Lai, W.S. and Carballo-Jane, E.
Ttp-related zinc finger domains and methods of use
Patent: WO 0112213-A 41 22-FEB-2001,
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
Location/Qualifiers
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Unclassified.
1 (bases 1 to 18)
Cowsert,L.M., Bennett,C.Frank. and O'Malley,B.W.
Antisense modulation of SRA expression
Patent: US 6107092-A 44 22-AUG-2000;
Location/Qualifiers
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1.9e+03;
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/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
0 c 0 g 18
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                 /organism="unknown"
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Best Local Similarity 100.0
Matches 17; Conservative
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source

FEATURES

BASE COUNT ORIGIN

DEFINITION ACCESSION VERSION KEYWORDS SOURCE

RESULT 3 AR106883

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ORGANISM

REFERENCE AUTHORS TITLE JOURNAL FEATURES

BASE COUNT ORIGIN

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Unknown.
Unclassified.
1 (bases 1 to 15)
Sullivan,S., Draper,K., Kisich,K., Stinchcomb,D.T. and McSwiggen,J.
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MUROS 40x 3.1 homeo gene 3'flank.
X12653 Y00215
X12653 Y00215
X12653 1 GI:51405
homeobox; Hox-3.1 gene.
Mus musculus (house mouse)
Mus musculus Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 48)
Le Moutellic, H., Condamine, H. and Brulet, P.
Pattern of transcription of the homeo gene Hox-3.1 in the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               see x12652 for Hox-3.1 gene 5' flank; see x07439 for Hox-3.1 cDNA sequence; the sequences are represented contiguously by [1]. Location/Qualifiers
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100.0%; Pred. No. 2.1e+04;
iive 0; Mismatches 0; Indels
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1 c 11 g 4 t
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Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 16; Conservative 0; Mismatches 0;
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AR041401
                             / organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1p36"
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/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
1.48
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88185818
                Location/Qualifiers
                                                                                                              /clone="pFU335R-S2"
/sex="male"
                                                                                                                                                                                                                                                                          378 AAAAATAAATAAA 393
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Brodeur,G.M.

Submission
Submitted (31-MAR-1994) Garrett M. Brodeur, Oncology, Children's
Hospital of Philadelphia, 34th and Civic Center Blvd, Philadelphia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

I (bases 1 to 48)

Brodeur, G.M.

FUCAl YAC FU335 right insert end sequence #2 of 2
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1 (bases 1 to 47)

1 (bases 1 to 47)

1 (bases 1 to 47)

Biallelic markers for use in constructing a high density disequilibrium map of the human genome

Patent: US 6537751-A 2541 25-MAR-2003;

Location/Qualifiers
                                         (Gases I to 47)
Cohen, D., Chumakov, I. and Blumenfeld, M.
Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
Patent: US 6537751-A 2343 25-MAR-2003;
Location/Qualifiers
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0.8%; Score 16; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 16; Conservative 0; Mismatches 0;
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0.8%; Score 16; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 16; Conservative 0; Mismatches 0;
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US 6537751.
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Sequence 2541 from patent
AR290806
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1 (bases 1 to 15)
Sullivan, S., Draper, K., Kisich, K., Stinchcomb, D.T. and McSwiggen, J.
TNF-.alpha. ribozymes
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Unclassified.
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Unclassified.
1 (bases 1 to 15)
Sullivan,S., Draper,K., Kisich,K., Stinchcomb,D.T. and McSwiggen,J.
Sullivan,S., Draper,B.
TNF- alpha. ribozymes
Patent: US 5811300-A 200 22-SEP-1998;
Location/Qualifiers
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Sullivan, S., Draper, K., Kisich, K., Stinchcomb, D.T. and McSwiggen, J.
TNF-alpha. ribozyma, 201 22-SEP-1998;
Location/Qualifiers
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100.0%; Pred. No. 8.2e+04;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 8.2e+04;
tive 0; Mismatches 0; Indels
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Sequence 200 from patent US 5811300.
AR041410
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Sequence 712 from patent US 5811300.
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1 (bases 1 to 15)
Sullivan,S., Draper,K., Kisich,K., Stinchcomb,D.T. and McSwiggen,J.
TNF-.alpha. ribozymes
Patent: US 5811300-A 192 22-SEP-1998;
Location/Qualifiers
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Sullivan,S., Draper,K., Kisich,K., Stinchcomb,D.T. and McSwiggen,J.
TNF-.alpha ribozymes
Patent: US 581130-A 199 22-SEP-1998,
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TNF-.alpha. ribozymes
Patent: US 5811300-A 191 22-SEP-1998;
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Sequence 199 from patent US 5811300.
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JOURNAL Patent: US 5811300-A 712 22-SEP-1998;
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Search completed: November 14, 2003, 16:27:36 Job time: 7539.5 secs

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November 14, 2003, 06:44:53 ; Search time 8568.5 Seconds (without alignments) 11258.085 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Name	00 - 0 - 1 - 1 - 1 - 2 - 2 - 3 - 3 - 3 - 3 - 3 - 3 - 3 - 3	Match	Lengt	m   00000	1 20000	Description A27635 JGMV coat p AX012654 Sequence AX088898 Sequence AX107024 Sequence AX177937 Sequence
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1 (bases 1 to 48)	RESULT 1 27635 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Scoat Scoat 5.1 etic etic ases		1 1 8	ALIGNMENTS 48 bp erminal oligom	inear PA

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PAT 14-FEB-2001

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1 (bases 1 to 30)
Lockerbie, R.Owen., Howard, M.L., Gallatin, W.Michael. and Lai, Y.
Modulators of anchoring protein function
Patent: US 6107104-A 45 22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.9%; Score 21; DB 6; Length 30;
100.0%; Pred. No. 5.3;
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Kwiatkowski,M., Landegren,U. and Nilsson,M. Solid phase synthesis
Patent: US 6313284-A 1 06-NOV-2001;
Location/Qualifiers
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AR177937/c
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Plant-derived resistance gene
Patent: Wo 9954490-A 49 28-OCT-1999;
BAULCOMBE DAVID CHARLES (GB); BENDAHWANE ABDELHAFID (GB); KANYUKA
KONSTANTIN VALERIEVICH (GB); PLANT BIOSCIENCE LIMITED (GB)
Location/Qualifiers
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Proline-rich extensin-like receptor kinases
Patent: WO 0114563-A 23 01-MAR-2001;
Goring, Daphne (CA); Silva, Nancy (CA)
Location/Qualifiers
            1. .48
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/organism="synthetic construct"
/mol_type="genomic DNA"
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/note="primer"
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Pred. No. 5.1;
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100.0%; Pred. No. ...
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Sequence 49 from Patent WO9954490.
AX012654
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Sequence 23 from Patent WO0114563.
AX088898
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PAT 27-AUG-2002

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16-JUN-1997 JP 1998501889
14-JUN-1996 US 08/663618
PATRICK W GRAY
C12N15/56,C12N9/24,C12N15/85,C12N5/10,C12N5/18,C07K16/40, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
JP 2001525821-A/1
11-DEC-2001
14-MAY-1998 JP 1998549151
14-MAY-1997 SE 9701783-4
MAREK KWIATKOWSKI, ULF LANDEGREN, MATS NILSSON
                   Length 30;
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unclassified.
1 (bases 1 to 30)
Kwiatkowski,M., Landegren,U. and Nilsson,M.
Synthesis of Oligonucleotides
Patent: JP 200155821-A 1 11-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                   Score 21; DB 6;
Pred. No. 5.3;
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llarity 100.0%; Pred. No. 5.3;
Conservative 0; Mismatches
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Patent: JP 2001510325-A 9 31-JUL-2001;
ICOS CORP
                 Query Match 0.9%; Score 21; DB Best Local Similarity 100.0%; Pred. No. 5.3 Matches 21; Conservative 0; Mismatches
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BD06115025-A/9.
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Synthesis of oligonucleotides.
BD085067
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Topology: Linear;
Key
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31-JUL-2001
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synthetic construct
artificial sequences.
1 (bases 1 to 30)
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PF 16-JU
PR 14-JU
PI PATRI
PC C12N1
A61K38/47
CC TOPOL
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BD064156/c
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Heller,M.J. and Tu,E.
DNA optical storage device using Forster energy transfer mechanism
Patent: US 6385080-A 15 07-MAY-2002;
Location/Qualifiers
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Gray,P.W.
Chitinase materials and methods
Patent: US 6372212-A 11 16-APR-2002;
Location/Qualifiers
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1 (bases 1 to 30)
Gray, P.W. and Tjoelker, L.W.
Chitimase chitin-binding fragments
Patent: US 6399571-A 11 04-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                30 bp
Sequence 15 from patent US 6385080.
AR209748
AR209748.1 GI:21511254
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Sequence 11 from patent US 6399571.
AR212146 GI:21515653
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 AR206049
AR206049.1 GI:21504535
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AR212146/c
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1 thases 1 to 32)
Kaluza, B., Betzl, G. and Weidle, U.H.
Antibody expression vector and antibodies produced thereby
BOEHRINGER MANNHEIM GMBH.
                                                                                                                                                                                                                                                                                 /organism='Artificial Sequence' Location/Qualifiers
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JP 2002315588-A/8
29-OCT-2002
02-NOV-2001 JP 2001337530
YOSHIZDMI ISHINO, KATSUYA DAIMON
C12N1S/09, C07K14/195, C12N15/00
Novel DNA polymerase accessory factor
Key
                                                                                 1 (bases 1 to 30)
Ishino, Y. and Daimon, K.
Novel DNA polymerase accessory factor
Patent: JP 2002315588-A 8 29-OCT-2002;
BIOMOLECULAR ENGINEERING RESEARCH INSTITUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. 32
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
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/organism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"
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BD178195
BD178195.1 GI:30015459
JP 2002315588-A/8.
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synthetic construct
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12-MAR-1998 US 09/039198

PATRICK W GRAY, LARRY W TJOBELKER

CI2NIS/09, A61K38/00, A61K38/46, A61K39/395, A61K45/00, A61P31/10,

CO7KL6/40,

CI2NI/15, CI2NI/19, CI2NI/21, CI2NS/10, C12N9/24, C12P21/08, G01N33/
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tive 0; Mismatches 0; Indels
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Description of Artificial Sequence: primer
Key
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C07H21/00,C07H21/02,C07H21/04
Synthesis of oligonucleotides
Key Location/Qualifiers
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artificial sequences.

(bases 1 to 30)
Caray. Pw. and Thoelker, L.W.
Chitin-binding fragment of chitinase
Patent: UP 2002505882-A 9 26-FEB-2002;
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Patent: US 6491908-A 4 10-DEC-2002;
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Stein, D.C. and Stover, C.K.
Vaccine delivery system
Patent: US 6180111-A 2 30-JAN-2001;
Location/Qualifiers
 Sequence 2 from patent US 6180111.
AR126240
AR126240.1 GI:14112833
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Sequence 4 from patent US 6491908.
AR264638 GI:29692909
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/organism="unknown"
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Rosenberg, A.S.
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